

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 12:02:57 ; Search time 338.08 Seconds  
(without alignments)  
2422.409 Million cell updates/sec

Title: US-09-763-498-7  
Perfect score: 477  
Sequence: 1 atggaaaagcattgaaat.....ggtaactactgctgttttaa 477

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_032802.\*  
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
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20: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	477	100.0	477	21	AAZ51247 Human Interleukin-
2	475.4	99.7	477	21	AAZ51248 Polymorphic human
3	461.2	96.7	819	22	AAD06911 Human interleukin-
4	349.8	73.3	391	22	AAF83870 Human interleukin-
5	238.6	50.0	809	19	AAV71960 Rodent interleukin
6	238.6	50.0	838	20	AAZ51246 CDNA encoding a mu
7	213	44.7	213	21	AAZ51246 3' exon of human I
8	202	42.3	1073	22	AAZ51246 Human interleukin-
9	202	42.3	1183	19	AAV42659 CDNA encoding Inte

10	202	42.3	1183	20	AAZ51247 Human interleukin-
11	202	42.3	1183	22	AAZ51247 Human cDNA encodin
12	202	42.3	1291	20	AAZ51247 Human cDNA encodin
13	201.6	42.3	673	22	AAZ51247 Human novel protei
14	201.6	42.3	673	22	AAZ51247 Human novel protei
15	201.4	42.2	1377	22	AAZ51247 Human cDNA encoding a hu
16	161.4	33.8	1321	21	AAZ51247 Human IL-1 recepto
17	161.4	33.8	1321	21	AAZ51247 Human IL-1 recepto
18	134.2	28.1	520	22	AAZ51247 Human IL-1 eta cDN
19	134.2	28.1	585	22	AAZ51247 Human Interleukin-
20	129.2	27.1	746	20	AAZ51247 Human Interleukin-
21	127	26.6	219	19	AAZ51247 Rodent interleukin
22	86.6	18.2	174	21	AAZ51247 Mouse interleukin-
23	78.8	16.5	1710	20	AAZ51247 Nucleotide sequenc
24	74.8	15.7	1877	21	AAZ51247 Mouse interleukin-
25	74.2	15.6	654	21	AAZ51247 Human zilla4 degen
26	72.6	15.2	654	21	AAZ51247 Human zilla4-E200K
27	71.8	15.1	531	22	AAZ51247 Nucleotide sequenc
28	71.8	15.1	531	22	AAZ51247 Nucleotide sequenc
29	71.8	15.1	603	22	AAZ51247 Equine interleukin
30	71.8	15.1	1577	19	AAZ51247 IL-1 inhibitor (IL
31	71.8	15.1	1614	22	AAZ51247 Recombinant human
32	70.8	14.8	456	14	AAZ51247 Recombinant human
33	70.8	14.8	462	18	AAZ51247 Plasmid 15424. Sy
34	70.8	14.8	462	19	AAZ51247 DNA encoding leade
35	70.8	14.8	462	19	AAZ51247 Leaderless IL-1 re
36	70.8	14.8	514	16	AAZ51247 Human interleukin-
37	70.8	14.8	514	18	AAZ51247 Human interleukin-
38	70.8	14.8	514	20	AAZ51247 Interleukin-1 rece
39	70.8	14.8	531	17	AAZ51247 Interleukin-1 rece
40	70.8	14.8	531	17	AAZ51247 Interleukin-1 rece
41	70.8	14.8	531	17	AAZ51247 IRAP gene. Homo s
42	70.8	14.8	531	17	AAZ51247 Sequence of bps 61
43	70.8	14.8	532	12	AAZ51247
44	70.8	14.8	540	10	AAZ51247
45	70.8	14.8			

ALIGNMENTS

RESULT	1
AAZ51247	
ID	AAZ51247 standard; DNA; 477 BP.
XX	AAZ51247;
AC	AAZ51247;
XX	06-JUN-2000 (first entry)
DT	Human Interleukin-1 epsilon DNA.
XX	Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
XX	immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW	gene mapping; immune system; treatment; inflammatory disease;
KW	autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW	psoriasis; human; ds.
XX	Homo sapiens.
OS	
XX	
FH	Key
FT	Location/Qualifiers
FT	1..477
FT	/tag= a
FT	/product= "Interleukin-1 epsilon protein"
FT	/note= "Homologous to mouse IL-1 epsilon protein"
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PN	WO200011174-A1.
XX	
PD	02-MAR-2000.
XX	
PF	20-AUG-1999; 99WO-US18771.
XX	
PR	21-AUG-1998; 98US-0097413.
PR	31-AUG-1998; 98US-0098595.

PR 11-SEP-1998; 98US-0099974.  
XX (IMMV ) IMMUNEX CORP.  
XX Sims JE, Smith DE;  
PI WPI: 2000-237653/20.  
XX P-PSDB; AAY70217.  
XX  
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
PT treat inflammatory and immune system-related diseases such as  
PT rheumatoid arthritis and inflammatory bowel disease -  
XX  
XX  
PS Claim 1a; Fig 1; 76pp; English.  
XX  
CC The present sequence is the human Interleukin-1 (IL-1) epsilon DNA  
CC encoding IL-1 epsilon protein. This gene is mapped to chromosome 2q and  
CC is mainly expressed in spleen, lymph node, thymus, tonsil and leucocyte  
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,  
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic  
CC activity. The DNA sequence can be used in chromosome identification,  
CC gene mapping and study of immune system. IL-1 epsilon can be used in the  
CC treatment of inflammatory or autoimmune diseases such as rheumatoid  
CC arthritis, inflammatory bowel disease and psoriasis.  
XX  
XX Sequence 477 BP; 124 A; 123 C; 117 G; 113 T; 0 other;

Query Match 100.0%; Score 477; DB 21; Length 477;  
Best Local Similarity 100.0%; Pred. No. 5.5e-137;  
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 atggaaaagcattgaaattgacacacctcagcagggagcattcaggatatacatcat 60  
Db 1 atggaaaagcattgaaattgacacacctcagcagggagcattcaggatatacatcat 60  
QY 61 cgggtgtgggtttcttcaggaccagcgtcatagcagtcctcagcaggaagcgtatgtct 120  
Db 61 cgggtgtgggtttcttcaggaccagcgtcatagcagtcctcagcaggaagcgtatgtct 120  
QY 121 ccagtcactattgccttaattcattcgcgcacatgtgagaccccttgagaagacagagg 180  
Db 121 ccagtcactattgccttaattcattcgcgcacatgtgagaccccttgagaagacagagg 180  
QY 181 aaccccatctactggcctgaatgagactcaatctcgtcgtatgtgtctaaagtcggg 240  
Db 181 aaccccatctactggcctgaatgagactcaatctcgtcgtatgtgtctaaagtcggg 240  
QY 241 gaccagccacactgcagctgaaggaaaggatataatgattgtgacaacaccccgag 300  
Db 241 gaccagccacactgcagctgaaggaaaggatataatgattgtgacaacaccccgag 300  
QY 301 cctgtgaagtctcttctctaccacagcagagtgaggaaactccacttcgagctc 360  
Db 301 cctgtgaagtctcttctctaccacagcagagtgaggaaactccacttcgagctc 360  
QY 361 gtggttccctcgtggttcctcgtcgtcagctctcgaaggaggtcgtcctcctcctt 420  
Db 361 gtggttccctcgtggttcctcgtcgtcagctctcgaaggaggtcgtcctcctcctt 420  
QY 421 acccaagaactgggggaaagcccaactactgactcttgggttaactatgctgttttaa 477  
Db 421 acccaagaactgggggaaagcccaactactgactcttgggttaactatgctgttttaa 477

## RESULT 2

AAZ51248  
ID AAZ51248 standard; DNA; 477 BP.

XX  
AC AAZ51248;

XX  
XX 06-JUN-2000 (first entry)

XX  
XX

DE Polymorphic human Interleukin-1 epsilon DNA.  
XX  
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;  
KW gene mapping; immune system; treatment; inflammatory disease;  
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
KW psoriasis; human; ds.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 1..477  
FT CDS  
FT /\*tag= a  
FT /product= "Interleukin-1 epsilon polymorphic variant"  
FT /note= "Homologous to mouse IL-1 epsilon protein"  
FT replace (35, A)  
FT /tag= b  
XX  
PN WO200011174-A1.  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-US18771.  
XX  
PR 21-AUG-1998; 98US-0097413.  
PR 31-AUG-1998; 98US-0098595.  
PR 11-SEP-1998; 98US-0099974.  
XX  
XX (IMMV ) IMMUNEX CORP.  
XX  
XX Sims JE, Smith DE;  
PI  
PI  
XX WPI: 2000-237653/20.  
DR P-PSDB; AAY70218.  
XX  
XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
PT treat inflammatory and immune system-related diseases such as  
PT rheumatoid arthritis and inflammatory bowel disease -  
XX  
XX  
PS Claim 1a; Fig 1; 76pp; English.  
XX  
CC The present sequence is the polymorphic human Interleukin-1 (IL-1)  
CC epsilon DNA. This gene is mapped to chromosome 2q and is mainly  
CC expressed in spleen, lymph node, thymus, tonsil and leucocyte  
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,  
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic  
CC activity. The DNA sequence can be used in chromosome identification,  
CC gene mapping and study of immune system. IL-1 epsilon can be used in the  
CC treatment of inflammatory or autoimmune diseases such as rheumatoid  
CC arthritis, inflammatory bowel disease and psoriasis.  
XX  
XX Sequence 477 BP; 123 A; 123 C; 118 G; 113 T; 0 other;

Query Match 99.7%; Score 475.4; DB 21; Length 477;  
Best Local Similarity 99.8%; Pred. No. 1.7e-136;  
Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 atggaaaagcattgaaattgacacacctcagcagggagcattcaggatatacatcat 60  
Db 1 atggaaaagcattgaaattgacacacctcagcagggagcattcaggatatacatcat 60  
QY 61 cgggtgtgggtttcttcaggaccagcgtcatagcagtcctcagcaggaagcgtatgtct 120  
Db 61 cgggtgtgggtttcttcaggaccagcgtcatagcagtcctcagcaggaagcgtatgtct 120  
QY 121 ccagtcactattgccttaattcattcgcgcacatgtgagaccccttgagaagacagagg 180  
Db 121 ccagtcactattgccttaattcattcgcgcacatgtgagaccccttgagaagacagagg 180  
QY 181 aaccccatctactggcctgaatgagactcaatctcgtcgtatgtgtctaaagtcggg 240  
Db 181 aaccccatctactggcctgaatgagactcaatctcgtcgtatgtgtctaaagtcggg 240

QY	241	gaccagccacactgcagctgaaggaaagataatggattgtacaacacccgag	300
Db	241	gaccagccacactgcagctgaaggaaagataatggattgtacaacacccgag	300
QY	301	ctgtggaagtcttctcttaccacagcagagtggcaggaactccaccttgcagtct	360
Db	301	ctgtggaagtcttctcttaccacagcagagtggcaggaactccaccttgcagtct	360
QY	361	gtggcttccctggctggctcgtctcagctctgaagcagagctctctctcatctt	420
Db	361	gtggcttccctggctggctcgtctcagctctgaagcagagctctctctcatctt	420
QY	421	accagaactggggaaagccaaactactgacttgggttaactctgctgttttaa	477
Db	421	accagaactggggaaagccaaactactgacttgggttaactctgctgttttaa	477
RESULT	3		
AAD06911			
ID	AAD06911	standard; cDNA; 819 BP.	
XX	AC		
XX	AC		
XX	AAD06911;		
XX			
XX	03-AUG-2001	(first entry)	
XX			
XX	Human interleukin-1	receptor antagonist-like (IL-lra-L) cDNA.	
DE			
XX	Human; interleukin-1	receptor antagonist-like protein; IL-lra-L; therapy;	
KW	rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;		
KW	joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;		
KW	transplant rejection; graft versus host disease; strain; sprain; leprosy;		
KW	cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;		
KW	clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;		
KW	myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;		
KW	acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;		
KW	eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;		
KW	hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;		
KW	infertility; endometriosis; retinal neuropathy; acute pancreatitis;		
KW	kawasaki's disease; cancer; ss.		
XX			
OS	Homo sapiens.		
XX			
XX	Key	Location/Qualifiers	
FH		1..819	
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FT		/*tag= a	
FT		/product= "Human interleukin-1 receptor antagonist-like	
FT		{IL-lra-L} protein"	
FT		/note= "CDS does not include stop codon"	
FT		/partial	
XX			
XX	WO200141792-A1.		
PN			
XX			
XX	14-JUN-2001.		
XX			
XX	04-DEC-2000;	2000WO-US32891.	
PF			
XX			
XX	10-DEC-1999;	99US-0170105.	
PR			
PR	28-NOV-2000;	2000US-0724859.	
XX			
XX	(AMGE-)	AMGEN INC.	
PA			
PA			
XX			
PI	Calzone FJ, Luethy R, Boedigheimer MJ, Zhu J, Chung Y, Jing S;		
XX			
XX	WPI; 2001-381495/40.		
DR			
DR	P-PSDB; AAE03417.		
XX			
PT	Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the		
PT	polypeptide encoded by the nucleic acid is useful diagnosis, treatment,		
PT	and prevention of diseases such as arthritis, diabetes, transplant		
PT	rejection -		
XX			
PS	Claim 1; Fig 1A; 127pp; English.		





Dd 462 gcagccttcctgggttggttcatcgctgctctctaaaggagctgccactattctg 521

Qy 421 acccaagaactgggaagccaacactactgacctgttggttaactatgcgttttaa 477  
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Dd 522 acccaagaactggggaaaacttcatacactgacttcgatgattgggtacattaa 578  
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RESULT 7  
AAZ51246  
ID AAZ51246 standard; DNA: 213 BP.  
XX  
AC AAZ51246;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE 3' exon of human Interleukin-1 epsilon DNA..  
XX  
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;  
KW gene mapping; immune system; treatment; inflammatory disease;  
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
KW psoriasis; human; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..213  
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FT FT /product= "Partial human IL-1 epsilon protein"  
FT FT /note= "Homologous to mouse IL-1 epsilon protein"  
XX  
PN WO200011174-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-US18771.  
XX  
PR 21-AUG-1998; 98US-0097413.  
PR 31-AUG-1998; 98US-0098595.  
PR 11-SEP-1998; 98US-0099974.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Sims JE, Smith DE;  
XX  
DR WFI: 2000-237653/20.  
DR P-PSDB; AAY70216.  
XX  
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
PT treat inflammatory and immune system-related diseases such as  
PT rheumatoid arthritis and inflammatory bowel disease -  
XX  
XX Claim la; Fig 1; 76pp; English.  
XX  
CC The present sequence is the 3' exon of human Interleukin-1 (IL-1)  
CC epsilon DNA. IL-1 epsilon gene is mapped to chromosome 2q and is mainly  
CC expressed in spleen, lymph node, thymus, tonsil and leucocyte tissues.  
CC IL-1 epsilon is a cytokine, with antiinflammatory, immunosuppressant,  
CC antirheumatic, antiarthritic and antipsoriatic activity. The DNA  
CC sequence can be used in chromosome identification, gene mapping and  
CC study of immune system. IL-1 epsilon can be used in the treatment of  
CC inflammatory or autoimmune diseases such as rheumatoid arthritis,  
CC inflammatory bowel disease and psoriasis.  
XX  
SQ Sequence 213 BP; 51 A; 56 C; 48 G; 58 T; 0 other;

Query Match 44.7%; Score 213; DB 21; Length 213;  
Best Local Similarity 100.0%; Pred.No. 9.3e-56;  
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 265 gaaagagataaatggattgtatacaaccacccgagcctgtgaagtctcttctcttac 324



Seq. ID	Accession	Length	Score	E-value	Identical	Mismatches	Indels	Gaps
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4	U00096.1	146	146	0.00	100	0	0	0
5	U00096.1	146	146	0.00	100	0	0	0
6	U00096.1	146	146	0.00	100	0	0	0
7	U00096.1	146	146	0.00	100	0	0	0
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10	U00096.1	146	146	0.00	100	0	0	0
11	U00096.1	146	146	0.00	100	0	0	0
12	U00096.1	146	146	0.00	100	0	0	0
13	U00096.1	146	146	0.00	100	0	0	0
14	U00096.1	146	146	0.00	100	0	0	0
15	U00096.1	146	146	0.00	100	0	0	0
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22	U00096.1	146	146	0.00	100	0	0	0
23	U00096.1	146	146	0.00	100	0	0	0
24	U00096.1	146	146	0.00	100	0	0	0
25	U00096.1	146	146	0.00	100	0	0	0
26	U00096.1	146	146	0.00	100	0	0	0
27	U00096.1	146	146	0.00	100	0	0	0
28	U00096.1	146	146	0.00	100	0	0	0
29	U00096.1	146	146	0.00	100	0	0	0
30	U00096.1	146	146	0.00	100	0	0	0
31	U00096.1	146	146	0.00	100	0	0	0
32	U00096.1	146	146	0.00	100	0	0	0
33	U00096.1	146	146	0.00	100	0	0	0
34	U00096.1	146	146	0.00	100	0	0	0
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47								

PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.

PR 28 JUN-2000; 2000US-0214000.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
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PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
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PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
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XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-476222/51.  
XX P-PSDB: AAU16937.  
XX Novel polypeptides and polynucleotides useful as diagnostic reagents to  
XX diagnose diseases or disorders associated with aberrant expression or  
XX activity of polypeptides, for treating blood clotting disorder,  
XX haemophilia  
XX Claim 1; SEQ ID No 34; 601pp; English.  
XX The invention relates to isolated nucleic acid molecules and their  
XX encoded secreted proteins. The nucleic acids and proteins are used to  
XX prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
XX rabbits, goats, horses, cats, dogs, chickens or sheep. They  
XX are also used in diagnosing a pathological condition or susceptibility  
XX to a pathological condition. Antibodies to the proteins can also  
XX be used in alleviating symptoms associated with the disorders and in





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Novel polypeptides and polynucleotides useful as diagnostic reagents to  
diagnose diseases or disorders associated with aberrant expression or  
activity of polypeptides, for treating blood clotting disorder,  
haemophilia -

PS Claim 1; SEQ ID No 107; 601pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage

CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
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OS Homo sapiens.

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Copyright (c) 1993 - 2000 Compugen Ltd.

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3	238.6	50.0	483	10	AF200493	AF200493 Mus muscu
4	238.6	50.0	795	10	AF206697	AF206697 Mus muscu
5	222	46.5	244	6	AX193660	AX193660 Sequence
6	215.8	45.2	197308	9	AC016724	AC016724 Homo sapi
7	202	42.3	1073	6	AX207820	AX207820 Sequence
8	202	42.3	1177	6	AF206696	AF206696 Homo sapi
9	202	42.3	1183	6	E54910	E54910 Interleukin
10	202	42.3	1183	6	AF200492	AF200492 Homo sapi
11	134.2	28.1	520	9	AX193587	AX193587 Sequence
12	134.2	28.1	585	6	AX052581	AX052581 Sequence
13	134.2	28.1	585	9	AF201833	AF201833 Homo sapi
14	134.2	28.1	1244	6	AX167128	AX167128 Sequence
15	129.2	27.1	746	6	AX137703	AX137703 Sequence
16	127	26.6	243	6	AX137705	AX137705 Sequence
17	127	26.6	294	6	AX137704	AX137704 Sequence
18	112	23.5	329	6	AX193643	AX193643 Sequence
19	106.4	22.3	186587	2	AC106686	AC106686 Rattus no
20	79.4	16.6	184626	2	AC096974	AC096974 Rattus no
21	78.8	16.5	1036	4	AY026462	AY026462 Canis fam
22	77.2	16.2	563	4	AF216526	AF216526 Canis fam
23	74.8	15.7	520	10	MUSILRA	M63100 M.musculus
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26	74.8	15.7	1576	10	MUSILIRAA	M57525 Mouse inter
27	74.8	15.7	1877	6	E55194	E55194 Interleukin
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36	71.2	14.9	197308	9	AC016724	AC016724 Homo sapi
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38	70.8	14.8	462	6	AR105636	AR105636 Sequence
39	70.8	14.8	474	6	A50276	A50276 Sequence 10
40	70.8	14.8	474	6	AR001464	AR001464 Sequence
41	70.8	14.8	474	6	AR055509	AR055509 Sequence
42	70.8	14.8	474	6	AR085392	AR085392 Sequence
43	70.8	14.8	514	6	I42450	I42450 Sequence 41
44	70.8	14.8	531	6	A49726	A49726 Sequence 1
45	70.8	14.8	531	6	A50144	A50144 Sequence 1

ALIGNMENTS

RESULT 1

AF201831

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

AF201831 Homo sapiens FIIL epsilon mRNA, complete cds.  
477 bp mRNA linear PRI 16-JAN-2000

AF201831.1 GI:6694389

human.

Human sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 477)

Smith,D.E., Renshaw,B.R., Ketchum,R.R., Kubin,M., Garka,K.E. and

Sims,J.E.

Four new members expand the interleukin-1 superfamily

J. Biol. Chem. 275 (2), 1169-1175 (2000)

20092888

2 (bases 1 to 477)

Sims,J.E.

Direct Submission

Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51

University Street, Seattle, WA 98101, USA

Location/Qualifiers

[illegible]



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VERSION      AX193660.1  GI:15211539
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
REFERENCE
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 244)
              Burgess, C.E., Prayaga, S.K., Shinkets, R.A., Rastelli, L.,
              Zerhusen, B.D., and Mezes, P.S.
              Proteins and nucleic acids encoding the same
              Patent: WO 0140291-A 82 07-JUN-2001;
              Curagen Corporation (US)
FEATURES
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1..244
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Matches 238; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

Qy 188 tctacctggcgctgaatgacctcaatctgcctgatgtgtgctaaagtctggggaccagc 247
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Qy 248 ccacactgcaactga-----aggaaaaggatataatggattgtatacaacaccccgagc 301
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Db 61 CCACACTGCACCTGAAGCTTCAGAGAAAGGATATAATGGATTGTATCAACCAACCCCGAGC 120

Qy 302 ctgtgaagtctcttctctaccacagcagagtgccaggaaactccacctcgagtcgtg 361
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Qy 362 tggcttccctggctggttcacgtcgtcagctctgagaggtgtgctctcctcattcctta 421
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Db 181 TGGCTTTCCCTGGCTGGTTTCATCGCTCTGACGCTGAGGAGGCTGTCTCTCATCCTTA 240

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RESULT      6
AC016724
LOCUS      AC016724 197308 bp DNA linear PRI 09-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-339F22 from 2, complete sequence.
ACCESSION  AC016724
VERSION    AC016724.11 GI:14718389
KEYWORDS  HTG.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 197308)
              Sulston, J.E. and Waterston, R.
              Toward a complete human genome sequence
              Genome Res. 8 (11), 1097-1108 (1998)
              99063792
MEDLINE
REFERENCE  2 (bases 1 to 197308)
              Armstrong, J. and Haakenson, W.
              The sequence of Homo sapiens BAC clone RP11-339F22
              Unpublished (2001)
JOURNAL
REFERENCE  3 (bases 1 to 197308)
              Waterston, R.H.
              Direct Submission
              Submitted (04-DEC-1999) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
              4 (bases 1 to 197308)
              Waterston, R.H.

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TITLE  
JOURNAL

Direct Submission  
Submitted (14-JUL-2001) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
5 (bases 1 to 197308)  
Waterston, R.  
Direct Submission  
Submitted (09-JAN-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Jul 14, 2001 this sequence version replaced gi:13431151.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc  
Contact: sapiens@watson.wustl.edu  
----- Summary Statistics  
-----  
Center project name: H\_NH0339F22  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

NOTICE: This sequence may not represent the entire insert of this  
clone. It may be shorter because we only sequence overlapping  
clone sections once, or longer because we provide a small overlap  
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by sequence  
from more than one subclone; and the assembly was confirmed by  
restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.  
McPherson, Department of Genetics, Washington University, St. Louis  
MO. For additional information about the map position of this  
sequence, see http://genome.wustl.edu/gsc

#### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male  
donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.,  
Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved  
approach for construction of bacterial artificial chromosome  
libraries. Genomics 51:1-8. The clone may be obtained either from  
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong  
and coworkers at the Roswell Park Cancer Institute  
(http://bacpac.med.buffalo.edu)

VECTOR: pBAC3.6

#### NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-725J3; the clone sequenced  
to the right is RP11-97J14. Actual start of this clone is at base  
position 1 of RP11-339F22; actual end is at base position 197308 of  
RP11-339F22.

Data from AC0844280 and AC024704 was used to finish this clone,  
AC016724. Polymorphisms have been identified between AC024704 and  
AC016724.

Sequence derived from pcr from base position 148683 to 149264.

FEATURES  
source

Location/Qualifiers  
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274..740  
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744..907  
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repeat\_region

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repeat_region 3235. .4195
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/rpt_family="MER1_type"
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repeat_region 8661. .8827
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Best Local Similarity 99.1%; Pred. No. 4.6e-54;
Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 259 ctgaaggaaaggatataatggattttgtacaacacccgagcctgtgaagtcctttctc 318
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Db 57056 CTTCAGGAAAGGATATATATGATTTGTACACCAACCCGAGCCTGTGAAGTCCTTTTC 57115

Qy 319 ttctaccacagcagtgaggagactccaccttcagctgtgcttccctggctgg 378
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Db 57116 TTCTACCACACGAGGAGGAGGAACCTCCACCTTCGAGCTGTGGCTTCCCTGGCTGG 57175

Qy 379 ttcacgtctcagctctgaaggaggtgtcctctcatcctaccacgaactgggaaa 438
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Db 57176 TTCATCGCTGTGAGTCTGAGGAGGCTGTCTCTCATCTTACCAAGAACTGGGAAA 57235

Qy 439 gccaacactactgactttgggttaactatgctgttttaa 477
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Db 57236 GCCAACACTACTGACTTTGGGTTAACTATGCTGTTTAA 57274

RESULT 7
LOCUS AX207820 1073 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 3 from Patent WO0157219.
ACCESSION AX207820
VERSION AX207820.1 GI:15422467
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1073)
AUTHORS Debets,J.E., Timans,J.C., Bazan,J.F. and Kastelein,R.A.
TITLE Mammalian interleukin-1-delta and -epsilon. Their use in
therapeutic and diagnostic methods
JOURNAL Patent: WO 0157219-A 3 09-AUG-2001;
SCHERING CORPORATION (US)
FEATURES
source
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67. .576
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 BASE COUNT 281 a 241 c 255 g 296 t  
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Query Match 42.3%; Score 202; DB 6; Length 1073;  
 Best Local Similarity 67.1%; Pred. No. 4.2e-50;  
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 Db 120 AATGTGTAACCTATTACTGGGACTATTAAATGATTGAATCAGCAAGTGTGGACCCCTTCA 179  
 QY 78 ggaccagcgtcatagcagtcgccgaggaagaccgtatgtctccagtcactattgcctt 137  
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 Db 240 TATCAGATGCAAGTATCCAGAGGCTCTTGAGCAAGGAGGAGGATCCCATTTATTGCG 299  
 QY 198 cctgaatggactcaatctctgcctgatgtgtctaaagtgcgggagccacactgca 257  
 Db 300 AATCAGAAATCCAGAAATGTGTTGATGTGAGAAAGTGTGGAGAACAGCCCATTTGCA 359  
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RESULT 8  
 AF206696 AF206696 1177 bp mRNA linear PRI 01-NOV-2001  
 LOCUS Homo sapiens interleukin-1 epsilon (IL1E) mRNA, complete cds.  
 DEFINITION  
 ACCESSION AF206696  
 VERSION AF206696.1 GI:11493847  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1177)  
 AUTHORS Debets,R., Timans,J.C., Homey,B., Zurawski,S., Sana,T.R., Lo,S.,  
 Wagner,J., Edwards,G., Clifford,T., Menon,S., Bazan,J.F. and  
 Kastelein,R.A.  
 TITLE Two novel IL-1 family members, IL-1 delta and IL-1 epsilon,  
 function as an antagonist and agonist of NF-kappa B activation  
 through the orphan IL-1 receptor-related protein 2  
 J. Immunol. 167 (3), 1440-1446 (2001)

JOURNAL MEDLINE 21359532  
 PUBMED 11466363  
 REFERENCE 2 (bases 1 to 1177)  
 AUTHORS Debets,R., Timans,J.C., Zurawski,S., Bazan,J.F. and Kastelein,R.A.  
 TITLE Direct Submission

JOURNAL Submitted (18-NOV-1999) Molecular Biology, DNAX Research Institute  
 of Molecular and Cellular Biology, Inc., 901 California Avenue,  
 Palo Alto, CA 94304-1104, USA

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 ORIGIN

Query Match 42.3%; Score 202; DB 9; Length 1177;  
 Best Local Similarity 67.1%; Pred. No. 4.3e-50;  
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 QY 78 ggaccagcgtcatagcagtcgccgaggaagaccgtatgtctccagtcactattgcctt 137  
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 QY 138 aatctatgccagcatgtgtgagacccttgagaagacagagggagcccaatctacctggg 197  
 Db 240 TATCAGATGCAAGTATCCAGAGGCTCTTGAGCAAGGAGGAGTTCCTCATTTATTGCG 299  
 QY 198 cctgaatggactcaatctctgcctgatgtgtctaaagtgcgggagccacactgca 257  
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 Db 360 GCTAAAGACGAGAAATCATGATCTGTATGCGCAACCCGAGCCCGTGAACCCCTTCT 419  
 QY 378 gttcatcgtctcagctcgaaggagcgtctcctctcattcattcccaagaactgggaa 437  
 Db 480 GTTCAT---TGCCCTCCTCAAGAGAGACCCAGCCCATCATTTCTGACTTTCAGAACTTGGGAA 536  
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 Db 537 GTCATACAACTGCGCTTGAATTAATAT 566  
 RESULT 9  
 E54910 E54910 1183 bp DNA linear PAT 07-FEB-2001  
 LOCUS Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide.  
 DEFINITION E54910  
 ACCESSION E54910.1 GI:13019313  
 KEYWORDS JP 2000032990-A/1.







SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 746)  
AUTHORS Busfield,S.J.  
TITLE Spoil-1 protein and nucleic acid molecules and uses therefor  
JOURNAL Patent: US 6197551-A 1 06-MAR-2001;  
FEATURES Location/Qualifiers  
source 1..746  
BASE COUNT 275 a 150 c 142 g 179 t  
ORIGIN

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Best Local Similarity 73.9%; Pred. No. 4.5e-28;  
Matches 164; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Db 390 GAAATCTTCATCATCAGTCTGAGATGATGTTGTGTACATTAA 431

Search completed: June 21, 2002, 11:56:23  
Job time: 15396 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 07:39:47 ; Search time 2781.56 Seconds  
(without alignments)  
1602.465 Million cell updates/sec

Title: US-09-763-498-5

Perfect score: 213

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*

30: em.htg.hum.\*

31: em.htg.inv.\*

32: em.htg.other.\*

33: em.htgo.inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
-----							

1	213	100.0	477	9	AF201831
2	213	100.0	197308	9	AC016724
3	175	82.2	391	6	AX193589
4	161	75.6	244	6	AX193660
5	125	58.7	483	10	AF200493
6	125	58.7	746	6	ARI37703
7	125	58.7	795	10	AF206697
8	122.8	57.7	243	6	ARI37705
9	122.8	57.7	294	6	ARI37704
10	106.4	50.0	186587	2	AC106686
11	97.4	45.7	1073	6	AX207820
12	97.4	45.7	1177	9	AF206696
13	97.4	45.7	1183	6	E54910
14	97.4	45.7	1183	9	AF200492
15	75.2	35.3	184626	2	AC096974
16	65.8	30.9	520	6	AX193587
17	65.8	30.9	585	6	AX052581
18	65.8	30.9	585	9	AF201833
19	65.8	30.9	1244	6	AX167128
20	65.8	30.9	197308	9	AC016724
21	64.6	30.3	329	6	AX193643
22	51	23.9	1036	4	AY026462
23	49.8	23.4	574	4	S68977
24	49.4	23.2	563	4	AF216526
25	48.8	22.9	465	6	AX080399
26	48.8	22.9	468	6	AX069335
27	48.8	22.9	471	10	AF230378
28	48.8	22.9	1283	10	AF200495
29	48.8	22.9	1284	6	AX080392
30	48.8	22.9	1284	10	MMU250429
31	48.6	22.8	218	6	AX193630
32	48.6	22.8	221	4	AF072476
33	48.6	22.8	531	6	AX127225
34	48.6	22.8	603	6	AX127227
35	48.6	22.8	1590	4	D83714
36	48.6	22.8	1590	6	E15594
37	48.6	22.8	1614	4	ECU92482
38	48.6	22.8	1614	6	AX127224
39	47.2	22.2	8032	6	AX069334
40	46.8	22.0	357	6	AX069304
41	46.8	22.0	465	6	AX080398
42	46.8	22.0	468	9	AF230377
43	46.8	22.0	985	6	AX069305
44	46.8	22.0	1025	6	AX207818
45	46.8	22.0	1282	6	AX069307

## ALIGNMENTS

RESULT 1

AF201831  
LOCUS AF201831 477 bp mRNA linear PRI 16-JAN-2000  
DEFINITION Homo sapiens FILL epsilon mRNA, complete cds.  
ACCESSION AF201831  
VERSION AF201831.1 GI:6694389  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 477)  
AUTHORS Smith,D.E., Renshaw,B.R., Ketchum,R.R., Kubin,M., Garika,K.E. and Sims,J.E.  
TITLE Four new members expand the interleukin-1 superfamily  
J. Biol. Chem. 275 (2), 1169-1175 (2000)  
MEDLINE 20092888  
REFERENCE 2 (bases 1 to 477)  
AUTHORS Sims,J.E.  
TITLE Direct Submission  
JOURNAL Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51 University Street, Seattle, WA 98101, USA  
FEATURES Location/Qualifiers

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/protein_id="AAF25211.1"
/db_xref="GI:6694390"
/translation="MEKALKIDPQGSIODINHRVWLQDOTLIAVPEKDRWSPVTI
ALISCRHVEFLDRGNPIYVLGLNGLMCAKVGDOPTLQLEKIDMLDINQPEPV
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BASE COUNT 124 a 123 c 117 g 113 t
ORIGIN

Query Match      100.0%; Score 213; DB 9; Length 477;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaaagataataagtgattgtacaaacacccgagcgtgtgaagtccttctctac 60
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Db 265 GAAAGGATATAATGATTGTACAAACACCCGAGCCTGTGAAGTCTTCTCTCTAC 324
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QY 61 cacacgaagtcgaggaactcacctcagctgtgcttccctggctggttcac 120
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Db 325 CACACCGAGTGGGAGGAACCTCCACTTCGAGTCTGTGGCTTCCCTGGCTGCATC 384
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QY 121 gctgcagctgtgaaggaggctcctctcatcctaccacaaagctgggaaagcacaac 180
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Db 385 GCTGTCAGCTCTGAAGGAGGCTGCTCTCATCTTACCACCAAGAACTGGGGAAGCCAAC 444
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QY 181 actactgacttgggttaactatcgtgtttaa 213
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Db 445 ACTACTGACTTGGGTTAACTATGCTGTTTAA 477
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RESULT 2
AC016724
LOCUS      AC016724      197308 bp      DNA      linear      PRI 09-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-339F22 from 2, complete sequence.
ACCESSION AC016724
VERSION   AC016724.11 GI:14718389
KEYWORDS  HTG.
SOURCE    human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 197308)
            Sulston, J.E. and Waterston, R.
            Toward a complete human genome sequence
            Genome Res. 8 (11), 1097-1108 (1998)
            99063792
REFERENCE 2 (bases 1 to 197308)
            Armstrong, J. and Haakenson, W.
            The sequence of Homo sapiens BAC clone RP11-339F22
            Unpublished (2001)
REFERENCE 3 (bases 1 to 197308)
            Waterston, R.H.
            Direct Submission
            Submitted (04-DEC-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            4 (bases 1 to 197308)
            Waterston, R.H.
            Direct Submission
            Submitted (14-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            5 (bases 1 to 197308)
            Waterston, R.

TITLE      Direct Submission
JOURNAL    Submitted (09-JAN-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
            On Jul 14, 2001 this sequence version replaced gi:13431151.
COMMENT    ----- Genome Center
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site: http://genome.wustl.edu/gsc
            Contact: sapiens@wustl.wustl.edu
            ----- Summary Statistics
            -----
            Center project name: H_NH0339F22
            -----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RP11-339F22 human BAC library was made from the blood of one male
donor, as described by Osogawa, K., Woon, P. Y., Zhao, B., Frengen, E.,
Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-725J3; the clone sequenced
to the right is RP11-97J14. Actual start of this clone is at base
position 1 of RP11-339F22; actual end is at base position 197308 of
RP11-339F22.

Data from AC084280 and AC024704 was used to finish this clone.
AC016724. Polymorphisms have been identified between AC024704 and
AC016724.

Sequence derived from pcr from base position 148683 to 149264.

FEATURES
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1. 197308
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone="RP11-339F22"
/clone_lib="RPC1-11"
/rep="2"
6. 275
/rpt_family="L1"
274. 740.
/rpt_family="L1"
744. 907
/rpt_family="ERV1"
917. 1361
/rpt_family="L1"
1362. 1814
/rpt_family="L1"
1838. 1952
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repeat_region 2245..2287
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repeat_region 2588..2877
/rpt_family="Alu"
repeat_region 2878..3244
/rpt_family="L1"
repeat_region 3235..4195
/rpt_family="L1"
repeat_region 3460..3481
/rpt_family="AT-rich"
repeat_region 4311..4450
/rpt_family="MIR"
repeat_region 4822..4957
/rpt_family="MER1_type"
repeat_region 5152..5337
/rpt_family="MER1_type"
repeat_region 6118..7901
/rpt_family="L2"
repeat_region 8008..8145
/rpt_family="L2"
repeat_region 8146..8343
/rpt_family="MER1_type"
repeat_region 8344..8429
/rpt_family="L2"
repeat_region 8601..8827
/rpt_family="ERV1"
repeat_region 8999..9029
/rpt_family="(T)n"
misc_feature 9003..9030
/note="similar to Homo sapiens EST BI091273
(NID:g14509603)"
misc_feature 9011..9031
/note="similar to Homo sapiens EST AA587127 (NID:g2397941)
n70c01.s1"
misc_feature 9013..9031
/note="similar to Homo sapiens EST AI034379 (NID:g3255332)
ox20g11.x1"
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/rpt_family="L2"
repeat_region 10187..10267
/rpt_family="MIR"
repeat_region 11074..11122
/rpt_family="(CTG)n"
repeat_region 11587..11611
/rpt_family="(TG)n"
repeat_region 11651..11884
/rpt_family="MaLR"
repeat_region 12198..12353
/rpt_family="MIR"
repeat_region 12578..12714
/rpt_family="MER1_type"
repeat_region 13540..13855
/rpt_family="Alu"
repeat_region 13985..14843
/rpt_family="L1"
repeat_region 14923..15243
/rpt_family="MER2_type"
repeat_region 15980..16836
/rpt_family="L1"
repeat_region 17526..17822
/rpt_family="Alu"
repeat_region 18067..18089
/rpt_family="AT-rich"
repeat_region 19365..19493
/rpt_family="MER1_type"
repeat_region 19604..20083
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repeat_region 22668..22977
/rpt_family="ERV1"
repeat_region 23349..23852
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/rpt_family="ERV1"
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Best Local Similarity 100.0%; Pred. No. 1e-55;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaaaaggataatggattgtacaacacccgagcctgtgagtccttctctctac 60
Db 57062 GAAAGGATATAGTATTGTACACCAACCCGAGCCTGTGAAGCTTCTCTCTAC 57121

QY 61 cacacccagagtcgaggaaactccacctcgagctgtgagcttccctcctcctc 120
Db 57122 CACACCCAGAGTCGAGCAACTCCACCTTCGAGTCTGTGGCTTTCCTGGGTTCATC 57181

QY 121 gctgtcagctctgaaggaggtgtcctctcctcctcctcctaccccaagaactgggaaagccaac 180
Db 57182 GCTGTCACTCTGAAGGAGGCTGTCTCTCATCTTACCCAGAACTGGGAAAGCCAAAC 57241

QY 181 actactgacttgggttaactatgtctgttttaa 213
Db 57242 ACTACTGACTTTGGGTTAACTATCTGTGTTAA 57274

RESULT 3
AX193589 391 bp DNA linear PAT 15-AUG-2001
LOCUS AX193589
DEFINITION Sequence 11 from Patent WO0140291.
ACCESSION AX193589
VERSION AX193589.1 GI:15211518
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 391)
AUTHORS Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L.,
Zerhusen,B.D. and Mezes,P.S.
TITLE Proteins and nucleic acids encoding the same
JOURNAL Patent: WO 0140291-A 11 07-JUN-2001;
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Location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 5.6e-44;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 gaaagagataatgattgtacacacacccagcctgtgaagtcctttcttctac 60  
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Db 217 GAAAGGATATAATGATTGTACAAACCAACCCGAGCCTGTGAAGCTCTTCTCTTCTAC 276  
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QY 61 cacagccagtgaggaggaactccacccctcagtgcttgccttccctggctggttcac 120  
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Db 277 CACAGCCAGAGTGGCAGGAATCCACCTCGAGTCTGTGGCTTCCCTGGCTGGTTCATC 336  
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QY 121 gctgcagctcgaagagctgtcctcctcctcctacccaagaactgggaaag 175  
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Db 337 CCTGTCAGCTCTGAAGAGGCTGCTCTCTCATCTTACCCAGAACTGGGGAAG 391  
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RESULT 4  
AX193660 AX193660 244 bp DNA linear PAT 15-AUG-2001  
LOCUS  
DEFINITION Sequence 82 from Patent WO0140291.  
ACCESSION AX193660  
VERSION AX193660.1 GI:15211539  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 244)  
AUTHORS Burgess,C.E., Prayaga,S.K., Shinkets,R.A., Rastelli,L.,  
Zerhusen,B.D. and Mezes,P.S.  
TITLE Proteins and nucleic acids encoding the same  
JOURNAL Patent: WO 0140291-A 82 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES  
Location/Qualifiers  
source 1..244  
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Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 84 GAAAGGATATAATGATTGTACAAACCAACCCGAGCCTGTGAAGCTCTTCTCTTCTAC 143  
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QY 61 cacagccagtgaggaggaactccacccctcagtgcttgccttccctggctggttcac 120  
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Db 144 CACAGCCAGAGTGGCAGGAATCCACCTCGAGTCTGTGGCTTCCCTGGCTGGTTCATC 203  
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QY 121 gctgcagctcgaagagctgtcctcctcctcctacccaagaactgggaaag 161  
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RESULT 5  
AF200493 AF200493 483 bp mRNA linear ROD 11-MAY-2000  
LOCUS  
DEFINITION Mus musculus interleukin-1 homolog 1 mRNA, complete cds.  
ACCESSION AF200493  
VERSION AF200493.1 GI:7769113  
KEYWORDS house mouse.  
SOURCE  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 483)  
AUTHORS Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N.,  
Griswold,D.E., Capper,E.A., Tal-Singer,R., Wells,G.I., Doyle,M.L.  
and Young,P.R.  
TITLE Identification and initial characterization of four novel members  
of the interleukin-1 family  
JOURNAL J. Biol. Chem. 275 (14), 10308-10314 (2000)

MEDLINE 20209405  
PUBMED 10744718  
REFERENCE 2 (bases 1 to 483)  
AUTHORS Kumar,S., McDonnell,P.C. and Young,P.R.  
TITLE Direct Submission  
JOURNAL Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,  
SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of  
Prussia, PA 19406, USA  
FEATURES  
Location/Qualifiers  
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CDS 1..483  
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Db 271 GAAGGGAACATATGGAATGTACACAAAGAACCTGTAAAGCCCTCTCTCTAT 330  
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QY 61 cacagccagtgaggaggaactccacccctcagtgcttgccttccctggctggttcac 120  
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Db 331 CACAAAGAGAGTGTGTACACACTCTACATTTGAGTCTGCAGCCTTCCCTGGTTCATC 390  
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QY 121 gctgcagctcgaagagctgtcctcctcctcctacccaagaactgggaaagccaac 180  
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Db 391 GCTGTCGCTCTAAGGGAGCTGCCCACTCATCTCTGACCCAGAACTGGGGAAATCTTC 450  
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QY 181 actactgacttgggttaactatgctggttttaa 213  
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Db 451 ATCACTGACTTCGAGATGATGTGGTTCATTAA 483  
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RESULT 6  
AR137703 AR137703 746 bp DNA linear PAT 16-JUN-2001  
LOCUS  
DEFINITION Sequence 1 from patent US 6197551.  
ACCESSION AR137703  
VERSION AR137703.1 GI:14479212  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 746)  
AUTHORS Busfield,S.J.  
TITLE Spoil-1 protein and nucleic acid molecules and uses therefor  
JOURNAL Patent: US 6197551-A 1 06-MAR-2001;  
Location/Qualifiers  
source 1..746  
/organism="unknown"  
BASE COUNT 275 a 150 c 142 g 179 t  
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Query Match 58.7%; Score 125; DB 6; Length 746;  
Best Local Similarity 74.2%; Pred. No. 2.6e-28;  
Matches 158; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY	1	gaaaggataataatggattgtacaaacaaacccgagcgtgtgaagtccctttctctac	60
Db	219	GAAGGGAACATAATGAAATGTACAACAAAAGGAACCTGTAAAAGCCTCTCTCTCTAT	278
QY	61	cacagccagagtgccaggaactccacccttcgagctgtggtcttccctggctgcattc	120
Db	279	CACAGAAGAGTGGTACAAACCTCTACATTTGAGTGTGAGCTGCCCTGGTGGTTCATC	338
QY	121	gctgtcagctgaaggaggtgctctcatccttaccagaactggggaagccaa	180
Db	339	GCTGTCTGCTCTAAAGGGAGCTGCCCACTCATCTGACCCAGAAGTGGGGAAATCTTC	398
QY	181	actaactgacttgggttaactatgctgttttaa	213
Db	399	ATCACTGACTTCGAGATGATTGTGTACATTAA	431

RESULT	7
AF206697	
LOCUS	Mus musculus interleukin-1 epsilon 795 bp mRNA linear ROD 01-NOV-2001
DEFINITION	AF206697
ACCESSION	AF206697.1 GI:11493849
VERSION	
KEYWORDS	
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 795) Debets,R., Timans,J.C., Homey,B., Zurawski,S., Sana,T.R., Lo,S., Wagner,J., Edwards,G., Clifford,T., Menon,S., Bazan,J.F. and Kastelein,R.A.
TITLE	Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kappa B activation through the orphan IL-1 receptor-related protein 2
JOURNAL	J. Immunol. 167 (3), 1440-1446 (2001)
MEDLINE	21359532
PUBMED	11466363
REFERENCE	2 (bases 1 to 795) Debets,R., Timans,J.C., Zurawski,S., Bazan,J.F. and Kastelein,R.A. Direct Submission
AUTHORS	Submitted (18-NOV-1999) Molecular Biology, DNAX Research Institute of Molecular and Cellular Biology, Inc., 501 California Avenue, Palo Alto, CA 94304-1104, USA
JOURNAL	
FEATURES	Location/Qualifiers
source	1..795 /organism="Mus musculus" /db_xref="taxon:10090" /chromosome="2" /map="proximal region; near Il1d" /dev_stage="17 day embryo" 1..795 /gene="Il1e" 76..558 /gene="Il1e" /note="interleukin-1-like protein; similar to IL-1a, IL-1b and IL-1ra; highly expressed in skin tissue; acts through an IL-1-like receptor IL-1Rrp2 resulting in IL-1-like signaling cascade; antagonized by IL-1d" /codon_start=1 /product="interleukin-1 epsilon" /protein_id="AAG35671.1" /db_xref="GI:11493850" /translation="MNKEILRAASPLRHVDLSRVWILONNLTAVPRKEQTPV TITLLFCQYLDLETRNGRDPDTMGVQRMSCFLCTKDGEPVQLQEGNIMEMYNKKE PVKASLFYHKSGTSTTFESAAPPFGWIAVCKSGSCPLITFLGELFITDFEMIVH "
gene	
CDS	

BASE COUNT	237 a	177 c	174 g	207 t
ORIGIN				

Query Match	58.7%	Score 125;	DB 10;	Length 795;
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AUTHORS	Busfield, S.J.
TITLE	Spoll-1 protein and nucleic acid molecules and uses therefor
JOURNAL	Patent: US 6197551-A 3 06-MAR-2001;
FEATURES	Location/Qualifiers
Source	1..294
BASE COUNT	86 a 68 c 66 g 74 t
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Query Match	57.7%; Score 122.8; DB 6; Length 294;
Best Local Similarity	74.8%; Pred No. 1.2e-27;
Matches 154; Conservative 0; Mismatches 52; Indels 0; Gaps 0;	
QY 1	gaaaggatataatggattgtcaacacccagcgtgtgaagtccttctctcttac 60
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RESULT 10  
 AC106686  
 LOCUS  
 DEFINITION  
 AC106686 186587 bp DNA linear HTG 12-JAN-2002  
 Rattus norvegicus clone CH230-62D13, \*\*\* SEQUENCING IN PROGRESS  
 \*\*\*, 85 unordered pieces.  
 AC106686  
 AC106686\_1 GI:181139210  
 HTG: HTGS\_PHASE1.  
 Norway rat.  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 186587)  
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-oshan,F.R., Allen,C.,  
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Weinstock,G. and Gibbs,R.

Direct Submission  
Unpublished  
2 (bases 1 to 186587)  
Worley,K.C.

Submitted  
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: GIUV  
Center clone name: CH230-62D13  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329First call to  
findhaplolist

Consensus quality: 13186 bases at least Q40  
Consensus quality: 144645 bases at least Q30  
Consensus quality: 154301 bases at least Q20  
Estimated insert size: 143906; sum-of-contigs estimation  
Quality coverage: 0x in Q20 bases; agarose-fp estimation  
Quality coverage: 1.9x in Q20 bases; sum-of-contigs estimation  
-----

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html))  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 85 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 3313: contig of 3313 bp in length  
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\* 3414 9926: contig of 6513 bp in length  
\* 9927 10026: gap of unknown length  
\* 10027 14917: contig of 4891 bp in length  
\* 14918 15017: gap of unknown length  
\* 15018 19779: contig of 4762 bp in length  
\* 19780 19879: gap of unknown length  
\* 19880 23114: contig of 3235 bp in length  
\* 23115 23214: gap of unknown length  
\* 23215 26939: contig of 3725 bp in length  
\* 26940 27039: gap of unknown length  
\* 27040 31422: contig of 4383 bp in length  
\* 31423 31522: gap of unknown length  
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\* 33706 33806: gap of unknown length  
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\* 36601 36700: gap of unknown length  
\* 36701 39809: contig of 3109 bp in length  
\* 39810 39909: gap of unknown length  
\* 39910 43147: contig of 3238 bp in length  
\* 43148 43248: gap of unknown length  
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\* 47077 47176: gap of unknown length  
\* 47177 49962: contig of 2786 bp in length  
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\* 50063 53178: contig of 3116 bp in length  
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\* 67418 67517: gap of unknown length  
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\* 72721 72820: contig of 2733 bp in length  
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\* 98403 98502: gap of unknown length  
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\* 100990 101089: gap of unknown length  
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Query Match 50.0%; Score 106.4; DB 2; Length 186587;  
Best Local Similarity 71.4%; Pred. No. 2.3e-22;  
Matches 140; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
Qy 18 ttgtacaaacccagcctgtgaagtccttctctctctaccacagccagagtgccag 77  
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Qy 78 gaactccacctcgagctgtggtttccctgggtggttcctgcgtcagctctgaagg 137  
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Qy 138 aggtgctctctcatccttaccacagaaactggggaagccacactactcttggtt 197  
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Db 171293 GACTGTAGTACATTAA 171308

RESULT 11  
AX207820 1073 bp DNA linear PAT 31-AUG-2001  
LOCUS AX207820  
DEFINITION Sequence 3 from Patent WO0157219.  
ACCESSION AX207820  
VERSION AX207820.1 GI:15422467  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 1073)  
AUTHORS Debets, J.E., Timans, J.C., Bazan, J.F. and Kastelein, R.A.  
TITLE Mammalian interleukin-1-delta and -epsilon. Their use in  
therapeutic and diagnostic methods  
JOURNAL Patent: WO 0157219-A 3 09-AUG-2001;  
SCHERING CORPORATION (US)  
FEATURES  
source  
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TAFELNIND"

CDS  
BASE COUNT 281 a 241 c 255 g 296 t  
ORIGIN  
Query Match 45.7%; Score 97.4; DB 6; Length 1073;  
Best Local Similarity 70.9%; Pred. No. 1.1e-19;

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Qy	121	gctgtcagctctgaaggagcgtgtctctctcactcttaccgaagactgggaaagccaac	180							
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RESULT 12	
AF206696	1177 bp mRNA linear PRI 01-NOV-2001
LOCUS	
DEFINITION	Homo sapiens interleukin-1 epsilon (IL1E) mRNA, complete cds.
ACCESSION	AF206696
VERSION	AF206696.1 GI:11493847
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1177)
	DeBELTS, R., TIMANS, J.C., HOMEY, B., ZURAWSKI, S., SANA, T.R., LO, S.,
	WAGNER, J., EDWARDS, G., CLIFFORD, T., MENON, S., BAZAN, J.F. and
	KASTALEIN, R.A.
TITLE	Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kappa B activation through the orphan IL-1 receptor-related protein 2
JOURNAL	J. Immunol. 167 (3), 1440-1446 (2001)

REFERENCE	2, (bases 1 to 1177)
AUTHORS	Debets P., Timans, J.C., Zurawski, S., Bazan, J.F. and Kastelein, R.A.
TITLE	Direct Submission
JOURNAL	Submitted (18-NOV-1999) Molecular Biology, DNAX Research Institute of Molecular and Cellular Biology, Inc., 501 California Avenue, Palo Alto, CA 94304-1104, USA
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CDS 67.1576

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BASE COUNT	320 a	249 c
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Query Match 45.7%;

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RESULT	13
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LOCUS	E54910
DEFINITION	Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide.
ACCESSION	E54910
VERSION	E54910.1 GI:13019313
KEYWORDS	JP 2000032990-A/1.
SOURCE	unidentified.
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 1183)
AUTHORS	Peter,R.Y.
TITLE	Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide
JOURNAL	Patent: JP 2000032990-A 1 02-FEB-2000;
	SMITHKLINE BEECHAM CORP
COMMENT	OS Unidentified
	PN JP 2000032990-A/1
	PD 02-FEB-2000
	PF 14-MAY-1999 JP 1999134172
	PR 28-JAN-1997 US 08/790032

PC	A61K31/00
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CC	Strandedness: Single;
CC	Topology: Linear;
FH	Key
FT	source
FT	Location/Qualifiers
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	/organism='Unidentified'.
FEATURES	Location/Qualifiers
source	1..1183
	/organism="unidentified"
	/db_xref="taxon:3264"
BASE COUNT	a 249 c 269 g 336 t

	Query Match	45.7%;	Score 97.4;	DB 6;	Length 1183;
	Best Local Similarity	70.9%;	Pred. No. 1.1e-19;		
	Matches 144;	Conservative	0;	Mismatches 56;	Indels 3;
					Gaps 1;
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Qy	61	caagccagagtgccaggaaactccaccttgactctgtggcttcctcgctgggttcac	120		
Db	435	CGTGCCAAGACTGGTAGGACCTCCACCCCTTGAGTCTGTGGCCTTCCCGGACTGGTTTCAT	- 493		
Qy	121	gctgtcagctctgaaggaggctgtcctctcatccttaccacaagaactggggaaagccac	180		

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58 unreplicated pieces.  
AC096974  
AC096974.3 GI:17975666  
HTG: HTGS\_PHASE1.  
Norway rat.  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 184626)  
Muzny D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,  
Alsbrooks, S.L., Amarantunga, H.C., Are, J.R., Banks, T., Barbaria, J.,  
Benton, J., Blmage, K., Blankenburg, K., Bonnin, D., Bouck, J.,  
Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,  
Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Cannon, T.F.,  
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,  
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,  
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,  
Davy-Carroll, J., Dederich, D.A., Delaney, K.R., Delgado, O.,  
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, R.J., Draper, H.,  
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,  
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Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,  
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Hollins, B., Honsi, F., Howard, S., Huber, J., Huiyk, S., Hume, J.,  
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Joudan, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,  
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,  
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,  
Loulsegh, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,  
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Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,  
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Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,  
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Quiles, M., Ren, Y., Rives, M., Rojbas, A., Rojubokan, F., Rolfe, N.,  
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N.,  
Sisson, I., Sodergren, E., Sonaite, T., Sparks, A., Stanley, H.,  
Stone, H., Sutton, A., Svatek, A., Taber, P., Tamerisa, A., Tamerisa, K.,  
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N.,  
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Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,  
Watlington, S., Williams, G., Williamson, A., Wleczky, R., Wooden, S.,  
Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,  
Weinstock, G. and Gibbs, R.  
Direct Submission  
Unpublished  
2 (bases 1 to 184626)  
Worley K.C.  
Direct Submission  
Submitted (05-OCT-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Dec 21, 2001 this sequence version replaced gi:17062392.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
-----  
Center project name: GGKC  
Center clone name: CH230-58p9  
----- Summary Statistics

Assembly program: Phrap; version 0.990329First call to findPhrapList

Consensus quality: 162978 bases at least Q40  
Consensus quality: 170371 bases at least Q30  
Consensus quality: 176254 bases at least Q20  
Estimated insert size: 168569; sum-of-contigs estimation  
Quality coverage: 0x in Q20 bases; agarose-fp estimation  
Quality coverage: 2.4x in Q20 bases; sum-of-contigs estimation

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\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hqsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hqsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently consists of 58 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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9609: gap of unknown length
9610: contig of 10685 bp in length
20294: gap of unknown length
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37161: contig of 4593 bp in length
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37262: contig of 6361 bp in length
43622: gap of unknown length
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43823: contig of 5800 bp in length
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35.3%; Score 75.2; DB 2; Length 184626;
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Matches 132; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

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Db 108474 AACATTCACCTTCAGTTTAGATATAAATTT 108447

Search completed: June 21, 2002, 11:56:00  
Job time: 15373 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 07:54:17 ; Search time 338.08 Seconds  
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1081.705 Million cell updates/sec

Title: US-09-763-498-5  
Perfect score: 213  
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Scoring table: IDENTITY\_NUC  
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Searched: 1736436 seqs, 858457221 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	100.0	213	21	AAZ51246
2	213	100.0	477	21	3' exon of human I
3	213	100.0	477	21	Human interleukin-
4	210	98.6	819	22	Polymorphic human
5	175	82.2	391	22	Human interleukin-
6	125	58.7	219	19	Human interleukin-
7	125	58.7	746	20	Rodent interleukin
8	125	58.7	809	19	CDNA encoding a mu
9	125	58.7	838	20	Rodent interleukin
					CDNA encoding a mu

10	97.4	45.7	1073	22	AAZ512296	Human interleukin-
11	97.4	45.7	1183	19	AAV42659	CDNA encoding inte
12	97.4	45.7	1183	20	AAZ90135	Human interleukin-
13	97.4	45.7	1183	22	AAZ26842	Human CDNA encodin
14	97.4	45.7	1291	20	AAZ86458	CDNA encoding a hu
15	97.4	45.7	1321	21	AAA96351	CDNA encoding a no
16	97.4	45.7	1321	21	AAA51595	Human IL-1 recepto
17	97.4	45.7	1377	20	AAZ86459	CDNA encoding a hu
18	97.4	45.7	1377	22	AAZ26915	Human CDNA encodin
19	97.4	45.7	673	22	AAZ16762	Human novel protei
20	65.8	30.9	520	22	AAZ83869	Human interleukin-
21	65.8	30.9	585	22	AAZ90487	Human IL-1 eta CDN
22	65.8	30.9	1244	22	AAZ08531	Human interleukin-
23	54.2	25.4	465	21	AAA09194	Human IL-1 homolo
24	54.2	25.4	465	21	AAA09195	Human IL-1 homolo
25	51	23.9	1710	20	AAV99953	Nucleotide sequenc
26	48.8	22.9	468	20	AAZ89431	Mouse interleukin
27	48.8	22.9	468	22	AAZ31373	Invention related
28	48.8	22.9	468	22	AAZ81700	Murine interleukin
29	48.8	22.9	470	19	AAV71958	Rodent interleukin
30	48.8	22.9	1275	21	AAZ09198	Murine IL-1 homolo
31	48.8	22.9	1284	22	AAZ27924	Murine IL-1 codi
32	48.8	22.9	1360	21	AAZ50811	Murine IL-1L1 codi
33	48.8	22.9	1385	21	AAZ51599	Murine TANGO-93 CD
34	48.6	22.8	531	22	AAZ85156	Murine IL-1 recept
35	48.6	22.8	603	22	AAZ85157	Nucleotide sequenc
36	48.6	22.8	1577	19	AAZ21578	Equine interleukin
37	48.6	22.8	1614	22	AAZ85155	Nucleotide sequenc
38	47.2	22.2	8032	22	AAZ31372	Invention related
39	46.8	22.0	357	22	AAZ31351	B2HFLS20W cDNA lib
40	46.8	22.0	358	20	AAZ30048	CDNA encoding a hu
41	46.8	22.0	468	20	AAZ89432	Human interleukin
42	46.8	22.0	468	21	AAA51597	Human IL-1 recepto
43	46.8	22.0	766	21	AAZ09193	Human IL-1 homolo
44	46.8	22.0	985	20	AAZ30049	CDNA encoding a hu
45	46.8	22.0	985	22	AAZ31352	B2HFLS20W cDNA lib

## ALIGNMENTS

RESULT 1  
AAZ51246  
ID AAZ51246 standard; DNA; 213 BP.

XX AAZ51246;

XX 06-JUN-2000 (first entry)

XX 3' exon of human Interleukin-1 epsilon DNA.

XX Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
XX immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;  
XX gene mapping; immune system; treatment; inflammatory disease;  
XX autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
XX psoriasis; human; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..213

XX /tag= a

XX /partial

XX /product= "Partial human IL-1 epsilon protein"

XX /note= "Homologous to mouse IL-1 epsilon protein"

XX WO200011174-A1.

XX 02-MAR-2000.

XX 20-AUG-1999; 99WO-US18771.

XX 21-AUG-1998; 98US-0097413.

XX

PR 31-AUG-1998; 98US-0098595.  
 PR 11-SEP-1998; 98US-0099974.  
 XX  
 PA (IMMV) IMMUNEX CORP.  
 XX Sims JE, Smith DE;  
 XX  
 DR WPI: 2000-237653/20.  
 DR P-PSDB: AAY70216.  
 XX  
 PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
 PT treat inflammatory and immune system-related diseases such as  
 PT rheumatoid arthritis and inflammatory bowel disease -  
 XX  
 PS Claim 1a; Fig 1; 76pp; English.  
 XX  
 CC The present sequence is the 3' exon of human Interleukin-1 (IL-1)  
 CC epsilon DNA. IL-1 epsilon gene is mapped to chromosome 2q and is mainly  
 CC expressed in spleen, lymph node, thymus, tonsil and leucocyte tissues.  
 CC IL-1 epsilon is a cytokine, with antiinflammatory, immunosuppressant,  
 CC antirheumatic, antiarthritic and antipsoriatic activity. The DNA  
 CC sequence can be used in chromosome identification, gene mapping and  
 CC study of immune system. IL-1 epsilon can be used in the treatment of  
 CC inflammatory or autoimmune diseases such as rheumatoid arthritis.  
 CC inflammatory bowel disease and psoriasis.  
 XX  
 SQ Sequence 213 BP; 51 A; 56 C; 48 G; 58 T; 0 other;

Query Match 100.0%; Score 213; DB 21; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 7e-59; Indels 0; Gaps 0;  
 Matches 213; Conservative 0; Mismatches 0;

QY 1 gaaaggataataaggattgtacacacccgagcgtggaagtccttctctac 60  
 |||||  
 DB 1 gaaaggataataaggattgtacacacccgagcgtggaagtccttctctac 60  
 QY 61 cacagccagagtgccaggaactccaccttgcctgctggtctccctggttcac 120  
 |||||  
 DB 61 cacagccagagtgccaggaactccaccttgcctgctggtctccctggttcac 120  
 QY 121 gctgtcagctctgaagagcgtctcctctcatcttaccacgaactgggaaagccaac 180  
 |||||  
 DB 121 gctgtcagctctgaagagcgtctcctctcatcttaccacgaactgggaaagccaac 180  
 QY 181 actactgacttgggttaactatgctgtttaa 213  
 |||||  
 DB 181 actactgacttgggttaactatgctgtttaa 213

RESULT 2  
 AAZ51247  
 ID AAZ51247 standard; DNA; 477 BP.  
 XX  
 AC AAZ51247;  
 XX  
 DT 06-JUN-2000 (first entry)  
 XX  
 DE Human Interleukin-1 epsilon DNA.  
 XX  
 KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
 KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;  
 KW gene mapping; immune system; treatment; inflammatory disease;  
 KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
 KW psoriasis; human; ds.  
 XX  
 OS Homo sapiens.  
 XX

Key Location/Qualifiers  
 CDS 1..477  
 FT /\*tag= a  
 FT /product= "Interleukin-1 epsilon protein"  
 FT /note= "Homologous to mouse IL-1 epsilon protein"

XX WO200011174-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US18771.  
 XX  
 PR 21-AUG-1998; 98US-0097413.  
 PR 31-AUG-1998; 98US-0098595.  
 PR 11-SEP-1998; 98US-0099974.  
 XX  
 PA (IMMV) IMMUNEX CORP.  
 XX Sims JE, Smith DE;  
 XX  
 DR WPI: 2000-237653/20.  
 DR P-PSDB: AAY70217.  
 XX  
 PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
 PT treat inflammatory and immune system-related diseases such as  
 PT rheumatoid arthritis and inflammatory bowel disease -  
 XX  
 PS Claim 1a; Fig 1; 76pp; English.  
 XX  
 CC The present sequence is the human Interleukin-1 (IL-1) epsilon DNA  
 CC encoding IL-1 epsilon protein. This gene is mapped to chromosome 2q and  
 CC is mainly expressed in spleen, lymph node, thymus, tonsil and leucocyte  
 CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,  
 CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic  
 CC activity. The DNA sequence can be used in chromosome identification,  
 CC gene mapping and study of immune system. IL-1 epsilon can be used in the  
 CC treatment of inflammatory or autoimmune diseases such as rheumatoid  
 CC arthritis, inflammatory bowel disease and psoriasis.  
 XX  
 SQ Sequence 477 BP; 124 A; 123 C; 117 G; 113 T; 0 other;

Query Match 100.0%; Score 213; DB 21; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-59;  
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaaaggataataaggattgtacacacccgagcgtggaagtccttctctac 60  
 |||||  
 DB 265 gaaaggataataaggattgtacacacccgagcgtggaagtccttctctac 324  
 QY 61 cacagccagagtgccaggaactccaccttgcctgctggtctccctggttcac 120  
 |||||  
 DB 325 cacagccagagtgccaggaactccaccttgcctgctggtctccctggttcac 384  
 QY 121 gctgtcagctctgaagagcgtctcctctcatcttaccacgaactgggaaagccaac 180  
 |||||  
 DB 385 gctgtcagctctgaagagcgtctcctctcatcttaccacgaactgggaaagccaac 444  
 QY 181 actactgacttgggttaactatgctgtttaa 213  
 |||||  
 DB 445 actactgacttgggttaactatgctgtttaa 477

RESULT 3  
 AAZ51248  
 ID AAZ51248 standard; DNA; 477 BP.  
 XX  
 AC AAZ51248;  
 XX  
 DT 06-JUN-2000 (first entry)  
 XX  
 DE Polymorphic human Interleukin-1 epsilon DNA.  
 XX  
 KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
 KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;  
 KW gene mapping; immune system; treatment; inflammatory disease;  
 KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
 KW psoriasis; human; ds.

```

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX DE CDS 1..477
XX FT /*tag= a
XX FT /product= "Interleukin-1 epsilon polymorphic variant"
XX FT /note= "Homologous to mouse IL-1 epsilon protein"
XX FT variation replace (35, A)
XX FT /*tag= b
XX PN WO200011174-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US18771.
XX PR 21-AUG-1998; 98US-0097413.
XX PR 31-AUG-1998; 98US-0098595.
XX PR 11-SEP-1998; 98US-0099974.
XX PA (EMV) IMMUNEX CORP.
XX PI Sims JE, Smith DE;
XX WPI; 2000-237653/20.
XX P-PSDB; AAY70218.
XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to
XX treat inflammatory and immune system-related diseases such as
XX rheumatoid arthritis and inflammatory bowel disease.
XX Claim 1a; Fig 1; 76pp; English.
XX The present sequence is the polymorphic human Interleukin-1 (IL-1)
XX epsilon DNA. This gene is mapped to chromosome 2q and is mainly
XX expressed in spleen, lymph node, thymus, tonsil and leucocyte
XX tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
XX immunosuppressant, antirheumatic, antithrombotic and antipsoriatic
XX activity. The DNA sequence can be used in chromosome identification,
XX gene mapping and study of immune system. IL-1 epsilon can be used in the
XX treatment of inflammatory or autoimmune diseases such as rheumatoid
XX arthritis, inflammatory bowel disease and psoriasis.
XX SQ Sequence 477 BP; 123 A; 123 C; 118 G; 113 T; 0 other;

Query Match 100.0%; Score 213; DB 21; Length 477;
Best Local Similarity 100.0%; Pred. No. 9.6e-59;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaaaggatataatgattgtacacacccgagcctgtgaagtccttcttctac 60
Dy 265 gaaaggatataatgattgtacacacccgagcctgtgaagtccttcttctac 324
QY 61 cacagccagtgaggaggaactccacttgcgtgtgcttccctggttcac 120
Dy 325 cacagccagtgaggaggaactccacttgcgtgtgcttccctggttcac 384
QY 121 gctgcagctcgaaggaggtgtctctctacacacacacacacacacacac 180
Dy 385 gctgcagctcgaaggaggtgtctctctacacacacacacacacacacac 444
QY 181 actactgacttgggttaactatgctgtttta 213
Dy 445 actactgacttgggttaactatgctgtttta 477

RESULT 4
AAD06911
ID RAD06911 standard; cDNA; 819 BP.
XX
AC AAD06911;

```

```

XX DT 03-AUG-2001 (first entry)
XX DE Human interleukin-1 receptor antagonist-like (IL-1ra-L) cDNA.
XX KW interleukin-1 receptor antagonist-like protein; IL-1ra-L; therapy;
XX KW rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;
XX KW joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;
XX KW transplant rejection; graft versus host disease; strain; sprain; leprosy;
XX KW cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;
XX KW clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;
XX KW myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;
XX KW acute respiratory disease syndrome; osteoporosis; Paget's disease; lymphoma;
XX KW hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;
XX KW infertility; endometriosis; retinal neuropathy; acute pancreatitis;
XX KW Kawasaki's disease; cancer; SS.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX DE CDS 1..819
XX FT /*tag= a
XX FT /product= "Human interleukin-1 receptor antagonist-like
XX FT (IL-1ra-L) protein"
XX FT /note= "CDS does not include stop codon"
XX FT /partial
XX PN WO200141792-A1
XX PD 14-JUN-2001.
XX PF 04-DEC-2000; 2000WO-US32891.
XX PR 10-DEC-1999; 99US-0170105.
XX PR 28-NOV-2000; 2000US-0724859.
XX PA (AMGE-) AMGEN INC.
XX PI Calzone FJ, Luethy R, Boedigheimer MJ, Zhu J, Chung Y, Jing S;
XX WPI; 2001-381495/40.
XX P-PSDB; AAE03417.
XX Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the
XX polypeptide encoded by the nucleic acid is useful diagnosis, treatment,
XX and prevention of diseases such as arthritis, diabetes, transplant
XX rejection.
XX Claim 1; Fig 1A; 127pp; English.
XX The present sequence is human interleukin-1 receptor antagonist-like
XX (IL-1ra-L) cDNA. IL-1ra-L is useful for treating, preventing or
XX ameliorating IL-1ra-L polypeptide-related disease, condition or disorder
XX which include rheumatoid arthritis, psoriatic arthritis, inflammatory
XX arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,
XX lupus, diabetes, transplant rejection, inflammatory joint disease, graft
XX versus host disease and inflammatory conditions resulting from strain,
XX sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human
XX immunodeficiency virus (HIV) infection, clostridium-associated
XX diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,
XX anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory
XX disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,
XX psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,
XX Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,
XX lymphomas, lung and breast cancer, leukaemias, infertility,
XX endometriosis, retinal degeneration, retinal neuropathy, acute
XX pancreatitis and Kawasaki's disease.
XX SQ Sequence 819 BP; 202 A; 196 C; 204 G; 217 T; 0 other;

Query Match 98.6%; Score 210; DB 22; Length 819;

```

Best Local Similarity 100.0%; Pred. No. 1.1e-57;  
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gaaagagataatgattgtacacacacccgagcctgtgaagtcctttcttctac 60  
|||||  
Db 610 gaaagagataatgattgtacacacacccgagcctgtgaagtcctttcttctac 669  
|||||  
Qy 61 cacagccagagtgagcaggaactccacccctcgagctgtggtttccctggctggttcac 120  
|||||  
Db 670 cacagccagagtgagcaggaactccacccctcgagctgtggtttccctggctggttcac 729  
|||||  
Qy 121 gctgcagctctgaagagagctgtctctcctccttaccacgaactggggaaagccaac 180  
|||||  
Db 730 gctgcagctctgaagagagctgtctctcctccttaccacgaactggggaaagccaac 789  
|||||  
Qy 181 actactgacttgggttaactatgctgttt 210  
|||||  
Db 790 actactgacttgggttaactatgctgttt 819  
|||||

RESULT 5  
AAF83870 ID AAF83870 standard; cDNA; 391 BP.  
XX AC AAF83870;  
XX DT 06-AUG-2001 (first entry)  
XX DE Human interleukin-1 receptor antagonist (NOVINTRA C) encoding cDNA.  
XX KW NOYX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;  
KW gonadotropin-like protein; NOVCON; interleukin-1; NOVINTRA; human;  
KW cytosolic; neuroprotective; reproductive; antiinflammatory; cancer;  
KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;  
KW antiasthmatic; antiallergic; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 1..391  
FT FT /\*tag= a  
FT FT /product= "NOVINTRA C"  
XX W0200140291-A2.  
XX PD 07-JUN-2001.  
XX PF 06-DEC-2000; 2000WO-US33029.  
XX PR 06-DEC-1999; 99US-0169056.  
XX PR 09-DEC-1999; 99US-0169866.  
XX PR 09-DEC-1999; 99US-0169886.  
XX PR 10-DEC-1999; 99US-0170252.  
XX PR 12-JAN-2000; 2000US-017540.  
XX PR 05-DEC-2000; 2000US-0170252.  
XX PA (CURA-) CURAGEN CORP.  
XX PI Burgess CE, Prayaga SK, Shimkets RA, Rastelli L, Zerhusen BD;  
PI Mezes PS;  
XX DR WPI; 2001-374790/39.  
XX DR P-PSDB; AAB85001.  
XX XX Novel isolated human transmembrane, neuromedin peptide  
PT gonadotropin-like protein and interleukin-1 receptor antagonist  
PT proteins, useful for treating cancer, immune response disorder,  
PT metabolic function disorders  
XX XX Claim 50; Fig 15A; 138pp; English.  
XX PS The invention provides novel polypeptides (NOYX) selected from human  
XX transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),  
CC

gonadotropin-like protein (NOVGON) and two interleukin-1 receptor  
CC antagonist proteins (NOVINTRA A and B). The invention also provides  
CC methods in which a NOYX polypeptide, polynucleotide and antibody are  
CC used in the detection, prevention and treatment of a broad range of  
CC pathological states. NOVTRAN can be used to treat a cell signaling  
CC disorder such as cancer, immune response disorder, hematopoietic  
CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat  
CC endocrine disorder, muscle disorder, neurologic disorder, cancers of  
CC central nervous system, breast, colon, ovary, kidney, prostate and  
CC thyroid. NOVCON can be used to treat reproductive development disorder,  
CC metabolic function disorder and melanoma. NOVINTRA A and B can be used  
CC to treat bone metabolism or structure disorder, inflammatory response  
CC disorder, immune regulation disorder, septic shock, stroke, diabetes,  
CC arthritis and cancer. The present sequence represents a cDNA encoding  
XX the NOVINTRA C polypeptide.

SQ Sequence 391 BP; 94 A; 106 C; 99 G; 92 T; 0 other;

Query Match 82.2%; Score 175; DB 22; Length 391;  
Best Local Similarity 100.0%; Pred. No. 1.5e-46;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gaaagagataatgattgtacacacacccgagcctgtgaagtcctttcttctac 60  
|||||  
Db 217 gaaagagataatgattgtacacacacccgagcctgtgaagtcctttcttctac 276  
|||||  
Qy 61 cacagccagagtgagcaggaactccacccctcgagctgtggtttccctggctggttcac 120  
|||||  
Db 277 cacagccagagtgagcaggaactccacccctcgagctgtggtttccctggctggttcac 336  
|||||  
Qy 121 gctgcagctctgaagagagctgtctctcctccttaccacgaactggggaaag 175  
|||||  
Db 337 gctgcagctctgaagagagctgtctctcctccttaccacgaactggggaaag 391  
|||||

RESULT 6  
AAV71959 ID AAV71959 standard; cDNA; 219 BP.  
XX AC AAV71959;  
XX DT 19-FEB-1999 (first entry)  
XX DE Rodent interleukin (IL)-1 epsilon partial polypeptide encoding cDNA.  
XX KW Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;  
KW inflammatory response; immune system; diagnosis; agonist; antagonist;  
KW chemokine; ss.  
XX OS Mus sp.  
XX FH Key Location/Qualifiers  
FT CDS 1..219  
FT FT /\*tag= a  
FT FT /product= "IL-1 epsilon polypeptide partial sequence"  
FT FT /note= "the start codon is not indicated"  
XX W09847921-A1.  
XX PD 29-OCT-1998.  
XX PF 17-APR-1998; 98WO-US06879.  
XX PR 06-AUG-1997; 97US-0055111.  
XX PR 21-APR-1997; 97US-0837627.  
XX XX (SCHE ) SCHERING CORP.  
XX PI Bazan JF, Hedrick JA, Kastelein RA, Sana TR;  
XX WPI; 1998-609976/51.  
XX DR P-PSDB; AAW86285.



```

XX 19-FEB-1999 (first entry)
XX
XX Rodent interleukin (IL)-1 epsilon polypeptide encoding cDNA.
XX
XX Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
XX inflammatory response; immune system; diagnosis; agonist; antagonist;
XX chemokine; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 90..578
XX /*tag= a
XX /product= "IL-1 epsilon polypeptide"
XX
XX W09847921-AL.
XX
XX 29-OCT-1998.
XX
XX 17-APR-1998; 98WO-US06879.
XX
XX 06-AUG-1997; 97US-0055111.
XX
XX 21-APR-1997; 97US-0837627.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Bazan JF, Hedrick JA, Kastelein RA, Sana TR;
XX
XX WPI; 1998-609976/31.
XX P-PSDB; AAW86286.
XX
XX Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
XX regulating the immune system and inflammatory responses
XX
XX Claim 14; Pages 92-93; 113pp; English.
XX
XX This cDNA encodes a rodent interleukin (IL)-1 epsilon polypeptide. The
XX invention relates to a recombinant polypeptide that specifically binds
XX polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
XX segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
XX IL polypeptides are used to regulate a cell involved in an inflammatory
XX response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
XX used to produce Abs and antigen-Abs complexes. The polypeptides, Abs and
XX the corresponding nucleic acids regulate development and/or the immune
XX system, and can be used to diagnose and treat conditions associated with
XX abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1
XX epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
XX IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
XX epsilon polypeptides may be used as a soluble polypeptide or as a fusion
XX protein with another cytokine or chemokine.
XX
XX Sequence 809 BP; 241 A; 180 C; 179 G; 209 T; 0 other;
XX
XX Query Match 58.7%; Score 125; DB 19; Length 809;
XX Best Local Similarity 74.2%; Pred. NO. 2.7e-30;
XX Matches 158; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
XX
Qy 1 gaaaggatataatggtttgtacaaacccgagcgtggaagctcttctctac 60
   ||| | ||||| ||||| ||| ||||| || ||||| ||| ||||| |||
Db 360 gaagggaacataatggaatgtacaaagaagacactgtataaagcctctctctat 419
   ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Qy 61 cacgacagagtgccaggaaactccacctgagctgtggtcttccctggctgttcac 120
   ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db 420 cacaagaagtggtacaaacctctacattgagctgcagcctccctgtgtgttcac 479
   ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Qy 121 gctgtcagctggaaggagctgtctctctatcctaccacaaagactggggaagcaac 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db 480 gctgtcgtctaaaggagctgcaccactattctgacccaagaactggggaatctc 539
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Qy 161 actactactgtgggttaactatgctgttttaa 213
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||

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Db 540 atcactgacttcgagatgattgtgtgtacattaa 572

#### RESULT 9

AAX86460

ID AAX86460 standard; CDNA; 838 BP.

XX AC AAX86460;

XX 30-SEP-1999 (first entry)

XX CDNA encoding a murine SPOIL-II protein.

DE SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;

XX bone metabolism disorder; proinflammatory disorder; immune disorder;

XX inflammatory disease; septic shock; stroke; diabetes; arthritis;

XX intercolitis; pneumonitis; epithelial cell; skin disease;

XX proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;

XX epithelial cancer; squamous cell carcinoma; bone resorption disorder;

XX osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;

XX osteogenesis imperfecta; fibrous dysplasia; hypophosphatasia;

XX bone sarcoma; myeloma bone disorder; osteolytic bone lesion;

XX hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;

XX bone fracture; ss.

XX Mus sp.

XX Key Location/Qualifiers

XX CDS 96..578

XX /\*tag= a

XX /product= SPOIL-II

XX W09937662-AL.

XX 29-JUL-1999.

XX 26-JAN-1999; 99WO-US01575.

XX 27-JAN-1999; 98US-0013810.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Busfield SJ;

XX WPI; 1999-458675/38.

XX P-PSDB; AAY24049.

XX New isolated SPOIL proteins, used to develop products for treating,

XX e.g. inflammatory and immune disorders

XX Claim 1; Fig 6; 126pp; English.

XX The present sequence encodes a SPOIL-II protein. The SPOIL proteins have

XX homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.

XX The SPOIL proteins are used as modulating agents in regulating a variety

XX of cellular processes. The products can be used for treating disorders

XX characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone

XX metabolism disorder, a proinflammatory disorder or an immune disorder.

XX They can be used for treating e.g. inflammatory diseases and disorders

XX e.g. inflammation, septic shock, stroke, diabetes, arthritis,

XX intercolitis and pneumonitis, epithelial cell and/or skin diseases and

XX disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma

XX and Kaposi's sarcoma and other epithelial cancers including squamous cell

XX carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and

XX bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's

XX disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,

XX fibrous dysplasia, hypophosphatasia, bone sarcoma, myeloma bone disorder

XX (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and

XX SPOIL modulators are useful for regulation of bone mass (e.g. increase in

XX bone mass and/or inhibit bone loss), management of bone fragility (e.g.

XX decrease bone fragility); and prevention and/or treatment of bone pain,

XX bone deformities and/or bone fractures. The products can also be used for

XX detection, diagnosis and screening assays.

XX  
SQ Sequence 838 BP; 256 A; 188 C; 184 G; 210 T; 0 other;

Query Match 58.7%; Score 125; DB 20; Length 838;  
Best Local Similarity 74.2%; Pred. NO. 2.7e-30;  
Matches 158; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 1 gaaagagataatggattgtacaacacccgagcctgtgagctctctctctac 60  
Dy 1 gaaagagataatggattgtacaacacccgagcctgtgagctctctctctac 60  
Db 366 gaaggagacataatggaatgtacaacaaaggaacccgtgaaagcctctctctat 425  
Qy 61 cacagcagagtgagcaggaactccaccttgcagctgtgagctctctctctac 120  
Dy 61 cacagcagagtgagcaggaactccaccttgcagctgtgagctctctctctac 120  
Db 426 cacagaagagtgagcaggaactccaccttgcagctgtgagctctctctctac 485  
Qy 121 gctgcagctgaagagagcgtctctctctctctctctctctctctctctac 180  
Dy 121 gctgcagctgaagagagcgtctctctctctctctctctctctctctctac 180  
Db 486 gctgctgctaaaggagcgtccacactctctctctctctctctctctctctct 545  
Qy 181 actactgacttgggttaactatgctgtttta 213  
Dy 181 actactgacttgggttaactatgctgtttta 213  
Db 546 atcactgacttcgagatgattggtacattaa 578

RESULT 10  
AAD12296  
ID AAD12296 standard; DNA; 1073 BP.  
XX  
AC AAD12296;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human interleukin-lepsilon (IL-lepsilon) protein DNA.  
KW Human; interleukin-lepsilon; IL-lepsilon; virucide; hepatotropic; fever;  
KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;  
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;  
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 67..576  
FT FT /\*tag= a  
FT FT /product= "Human interleukin-lepsilon (IL-lepsilon)  
FT FT protein"  
XX  
PN WO200157219-A2.  
XX  
PD 09-AUG-2001.  
XX  
XX 01-FEB-2001; 2001WO-US03285.  
XX  
XX 02-FEB-2000; 2000US-0179638.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Debets JEMA, Timans JC, Bazan JF, Kastelein RA;  
XX  
XX WPI: 2001-488886/53.  
XX  
XX P-PSDB: AAE06656.  
XX  
XX Novel isolated or recombinant antigenic interleukin-1 delta or epsilon  
XX polypeptide useful for treating conditions exhibiting abnormal  
XX expression of interleukin such as immunological disorders, tumor and  
XX allergy  
XX  
XX Claim 18; Page 86-87; 103pp; English.  
XX  
XX The invention relates to recombinant antigenic interleukin-1 like  
XX molecules and their corresponding nucleic acid sequences, designated  
XX as interleukin-1delta (IL-1delta) and interleukin-lepsilon (IL-lepsilon).

IL-1delta and IL-lepsilon are useful for treating conditions exhibiting abnormal expression of the interleukin such as immunological disorders, tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis, allergy, autoimmune diseases and infectious diseases (e.g., pulmonary tuberculosis, leprosy, fulminant hepatitis, and viral infections such as HIV). The invention also relates to methods of using the composition containing IL-1delta or IL-lepsilon for both diagnostic and therapeutic utilities. IL-1delta is used as an immunogen for the production of antiserum or antibodies specific, e.g., capable of distinguishing between IL-1 family members and an IL-1delta, for the interleukin or its fragment. The purified interleukin is used as a reagent to detect any antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous cytokine. The invention also contemplates the use of competitive drug screening assays. The present DNA sequence encodes human interleukin-lepsilon (IL-lepsilon) protein.

SQ Sequence 1073 BP; 281 A; 241 C; 255 G; 296 T; 0 other;

Query Match 45.7%; Score 97.4; DB 22; Length 1073;  
Best Local Similarity 70.9%; Pred. NO. 2.3e-21;  
Matches 144; Conservative 0; Mismatches 56; Indels 3; Gaps 1

Qy 1 gaaagagataatggattgtacaacacccgagcctgtgagctctctctctac 60  
Dy 1 gaaagagataatggattgtacaacacccgagcctgtgagctctctctctac 60  
Db 367 gagcagaagatcgtatgctgagcagccgagccgtgaaacccctctctctac 426  
Qy 61 cacagcagagtgagcaggaactccaccttgcagctgtgagctctctctctac 120  
Dy 61 cacagcagagtgagcaggaactccaccttgcagctgtgagctctctctctac 120  
Db 427 cgtgccagagctgtagcagcctccaccccttgagctgtgagctctctctctac 485  
Qy 121 gctgcagctgaagagagcgtctctctctctctctctctctctctctctac 180  
Dy 121 gctgcagctgaagagagcgtctctctctctctctctctctctctctctac 180  
Db 486 --tgcctcctcaagagagacccacccatctctgactcgaactcgggaagcctac 543  
Qy 181 actactgacttgggttaactat 203  
Dy 181 actactgacttgggttaactat 203  
Db 544 aacactgccttgaattaaat 566

RESULT 11  
AAV42659  
ID AAV42659 standard; cDNA; 1183 BP.  
XX  
AC AAV42659;  
XX  
DT 14-OCT-1998 (first entry)  
XX  
DE cDNA encoding Interleukin-1 receptor antagonist beta (IL-lra-beta).  
XX  
KW Interleukin-1 receptor antagonist beta; IL-lra-beta; IL-1 alpha;  
KW IL-1 beta; inflammatory response; treatment; inflammation; septicaemia;  
KW cancer; anaemia; arthritis; inflammatory bowel disease;  
KW graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;  
KW acute respiratory disease syndrome; psoriasis; restenosis;  
KW traumatic brain injury; acquired immune deficiency syndrome;  
KW cachexia; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 75..584  
FT FT /\*tag= a  
FT FT /product= IL-lra-beta  
XX  
PN EP855404-A1.  
XX  
PD 29-JUL-1998.  
XX  
XX 27-JAN-1998; 98EP-0300572.  
XX  
XX 28-JAN-1997; 97US-0790032.  
XX

XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX Young PR;  
XX WPI: 1998-389778/34.  
XX P-PSDB; AAW63136.  
XX New nucleic acid encoding human interleukin-1 receptor antagonist  
PT beta polypeptides - and related expression systems, transformed  
PT cells, proteins, antibodies, agonists and antagonists, useful for  
PT treatment, prevention and diagnosis of inflammation, septicemia,  
PT cancer etc  
XX  
XX Claim 3: Fig 1: 20pp; English.  
XX  
XX The present sequence encodes human Interleukin-1 receptor antagonist  
CC beta (IL-1ra-beta). IL-1 alpha and IL-1 beta play key roles in  
CC inflammatory responses, and are produced as zymogens which are cleaved  
CC upon secretion to yield mature carboxyl terminal 17 kD fragments.  
CC IL-1ra-beta polypeptides and polynucleotides are useful in treatment of  
CC chronic and acute inflammation, septicemia, cancer, anaemia, arthritis,  
CC inflammatory bowel disease, graft vs. host rejection, autoimmunity,  
CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),  
CC psoriasis, restenosis, traumatic brain injury, acquired immune  
CC deficiency syndrome (AIDS) and cachexia. These conditions (or  
CC susceptibility to them) may be diagnosed by detecting mutations in the  
CC IL-1ra-beta coding sequence analysing a sample for presence or amount  
CC of IL-1ra-beta.  
XX  
XX Sequence 1183 BP; 329 A; 249 C; 269 G; 336 T; 0 other;  
XX  
Query Match 45.7%; Score 97.4; DB 19; Length 1183;  
Best Local Similarity 70.9%; Pred. No. 2.4e-21;  
Matches 144; Conservative 0; Mismatches 56; Indels 3; Gaps 1;  
QY 1 gaaaagataatgattgtacacacccgagcctgtgagtccttctctctac 60  
DB 375 gagcagaagatcgtatgtatgccaacccgagccgagacccctctctctac 434  
QY 61 cacagccagagtgccaggaactccacttcgagctgtggtcttccctgggtggtc 120  
DB 435 cgtgccaagactgtgagaccccttcgagctgtggtcttccctgggtggtc 493  
QY 121 gctgtcagctctgaagagaggtgtctctctctctctctctctctctctctac 180  
DB 494 --tgctctctccaagagagagacccatctctgacttcagaaacttgggaagtcatac 551  
QY 181 actactgacttgggttaactat 203  
DB 552 aacactgctcttgaattaataat 574  
RESULT 12  
AAX90135  
ID AAX90135 standard; cDNA; 1183 BP.  
XX  
AC AAX90135;  
XX  
DT 20-SEP-1999 (first entry)  
XX  
DE Human interleukin-1 receptor antagonist beta encoding cDNA.  
XX  
KW Human; interleukin-1 receptor antagonist beta; IL-1ra-beta; septicemia;  
KW chronic inflammation; acute inflammation; arthritis; autoimmunity;  
KW inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;  
KW cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;  
KW traumatic brain injury; AIDS; cachexia; allergy; parasite infection;  
KW allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;  
KW allergic inflammatory disease; delayed hypersensitivity; vaccine; ss.  
XX  
OS Homo sapiens.

XX WO9936541-A1.  
XX 22-JUL-1999.  
XX  
XX 14-JAN-1999; 99WO-US00847.  
XX  
XX 29-APR-1998; 98US-0069619.  
XX 14-JAN-1998; 98US-0007464.  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX Marshall L, Young PR;  
XX WPI: 1999-430615/36.  
XX P-PSDB; AAY24395.  
XX New interleukin-1 receptor antagonist beta, useful for treating  
PT inflammation and autoimmune diseases  
XX  
XX Claim 5: Fig 1: 34pp; English.  
XX  
XX The present sequence encodes human interleukin-1 receptor antagonist  
CC beta (IL-1ra-beta). IL-1ra-beta polypeptides and polynucleotides are  
CC useful for diagnosing diseases (or susceptibility to diseases) related  
CC to the expression or activity of IL-1ra-beta, by determining mutations  
CC in the IL-1ra-beta nucleic acid sequences and/or analysing for the  
CC presence or amount of IL-1ra-beta polypeptide. IL-1ra-beta polypeptides  
CC are also useful for screening for compounds which affect activity of the  
CC protein. These can be used in treatment to inhibit (antagonist) or  
CC enhance (agonist) IL-1ra-beta activity, in addition to direct  
CC administration of IL-1ra-beta polypeptides to treat conditions, or  
CC direct administration of antisense sequences to prevent expression.  
CC IL-1ra-beta polypeptides (administered directly, in a vector i.e. gene  
CC therapy, and as a vaccine) and antibodies induce an immune response to  
CC immunise and prevent disease. Diseases diagnosed, prevented or treated  
CC include chronic and acute inflammation, septicemia, arthritis,  
CC inflammatory bowel disease, graft vs. host disease, autoimmunity,  
CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),  
CC psoriasis, restenosis, traumatic brain injury, AIDS, cachexia, allergy,  
CC parasite infection, allergic rhinitis, allergic asthma, atopic  
CC dermatitis, allergic inflammatory diseases and delayed hypersensitivity.  
XX  
XX Sequence 1183 BP; 329 A; 249 C; 269 G; 336 T; 0 other;  
XX  
Query Match 45.7%; Score 97.4; DB 20; Length 1183;  
Best Local Similarity 70.9%; Pred. No. 2.4e-21;  
Matches 144; Conservative 0; Mismatches 56; Indels 3; Gaps 1;  
QY 1 gaaaagataatgattgtacacacccgagcctgtgagtccttctctctac 60  
DB 375 gagcagaagatcgtatgtatgccaacccgagccgagacccctctctctac 434  
QY 61 cacagccagagtgccaggaactccacttcgagctgtggtcttccctgggtggtc 120  
DB 435 cgtgccaagactgtgagaccccttcgagctgtggtcttccctgggtggtc 493  
QY 121 gctgtcagctctgaagagaggtgtctctctctctctctctctctctctac 180  
DB 494 --tgctctctccaagagagacccatctctgacttcagaaacttgggaagtcatac 551  
QY 181 actactgacttgggttaactat 203  
DB 552 aacactgctcttgaattaataat 574  
RESULT 13  
AAS26842  
ID AAS26842 standard; cDNA; 1183 BP.  
XX  
AC AAS26842;  
XX

DT 07-NOV-2001 (first entry)  
XX Human cDNA encoding a novel secreted protein, SEQ ID 34.  
DE  
XX  
XX  
KW Human; immunosuppressive; antiarthritic; ss; antirheumatic;  
KW cytosolic; cardiant; vasotropic; cerebroprotective; nootropic;  
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
KW vulnary; secreted protein; rheumatoid arthritis;  
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
KW corneal infection; wound healing; epithelial cell proliferation;  
KW skin ageing; food additive; preservative; antiproliferative.  
XX  
OS Homo sapiens.  
XX  
XX W0200155441-A2.  
PN  
XX  
XX 02-AUG-2001.  
PD  
XX  
XX 17-JAN-2001; 2001WO-0501320.  
PF  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 01-NOV-2000; 2000US-0241826.  
PR 08-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.



Query Match 45.7%; Score 97.4; DB 20; Length 1291;  
Best Local Similarity 70.9%; Pred. No. 2.5e-21;  
Matches 144; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

QY 1 gaaagagataatgattgtacaacaccggcctgtgaacttccttctttcttac 60  
|| || || || || || || || || || || || || || || || || || || ||  
Db 424 gagcagaagatcatgatctgtatgcccaaccggccgtgaaaccttctttcttac 483  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 61 cacagccagagtggcgaggaaactccaccttcgagctgtgtggctttcccttggttcac 120  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 484 cgtgcgaagactgttaggacctccaccttcgagctgtgtggctttcccgactggttcac - 542

QY 121 gctgtcagctctgaagaggctgtctcttccttccttcacccaagaactggggaagccaac 180  
|| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 543 --tgcctcctccaagagaccagcccattcttgacttcagaacttgggaagtcatac 600

QY 181 actactgactttgggttaactat 203  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 601 aacactgcctttgaattaatat 623

RESULT 15  
ID AAA96351 standard; cDNA; 1321 BP.  
XX  
AC AAA96351;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE cDNA encoding a novel polypeptide designated PRO5737.

XX KW Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;  
PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;  
KW PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;  
KW PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;  
KW Insulinemia; kidney disorder; Bergers disease; nephropathy;  
KW Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;  
Crohns disease; ss.  
XX  
OS Homo sapiens.

PH Key Location/Qualifiers  
FT CBS 96..500 /tag= a  
FT sig\_peptide 96..146 /\*tag= b  
FT FT  
XX WO200056889-A2.  
XX  
XX 28-SEP-2000.  
XX  
XX 01-MAR-2000; 2000WO-US05601.  
XX  
XX 23-MAR-1999; 99US-0125774.  
PR 23-MAR-1999; 99US-0125778.  
PR 24-MAR-1999; 99US-0125826.  
PR 31-MAR-1999; 99US-0127035.  
PR 05-APR-1999; 99US-0127706.  
PR 21-APR-1999; 99US-0130359.  
PR 27-APR-1999; 99US-0131270.  
PR 27-APR-1999; 99US-0131272.  
PR 04-MAY-1999; 99US-0131291.  
PR 04-MAY-1999; 99US-0132371.  
PR 04-MAY-1999; 99US-0132379.  
PR 04-MAY-1999; 99US-0132383.  
PR 25-MAY-1999; 99US-0135750.  
PR 08-JUN-1999; 99US-0138166.  
PR 20-JUL-1999; 99US-0144791.  
PR 03-AUG-1999; 99US-0146970.  
PR 09-DEC-1999; 99US-0170262.  
XX  
XX (GETH ) GENENTECH INC.

Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
WPI: 2000-628263/60.  
P-PSDB; AAB18924.  
Novel secreted and transmembrane polypeptides useful for diagnosing  
tumour in a mammal, for identifying agonists and antagonists of the  
polypeptide and for therapeutic use -  
Claim 2; Fig 31; 222pp; English.  
The present sequence encodes a secreted or transmembrane polypeptide.  
The specification describes polypeptides designated PRO1484, PRO4334,  
PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,  
PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,  
PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is  
useful for diagnosing tumour in a mammal. The polypeptides, their  
agonists and antagonists are useful treating a condition associated with  
expression or activity of the polypeptide. Conditions treated include  
obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are  
capable of inducing proliferation of mammalian kidney mesangial cells  
and are therefore useful for treating kidney disorders associated with  
decreased mesangial cell function such as Bergers disease or other  
nephropathies associated with Schonlein-Henoch purpura, celiac disease,  
dermatitis herpetiformis or Crohns disease. The nucleic acids may be used  
to generate transgenic animals for use in development and screening of  
therapeutically useful reagents and also for chromosome identification  
and tissue typing.

Sequence 1321 BP; 362 A; 278 C; 293 G; 388 T; 0 other:  
Query Match 45.7%; Score 97.4; DB 21; Length 1321;  
Best Local Similarity 70.9%; Pred. No. 2.5e-21;  
Matches 144; Conservative 0; Mismatches 56; Indels 3; Gaps 1;  
QY 1 gaaaaggatataaatgattgtgtacaaacccgagcctgtgaaacttccttctttcttac 60  
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Db 291 gagcagaagatcatgatctgtatgcccaaccggccgtgaaaccttctttcttac 350

QY 61 cacagccagagtggcgaggaaactccaccttcgagctgtgtggctttcccttggttcac 120  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 351 cgtgcgaagactgttaggacctccaccttcgagctgtgtggctttcccgactggttcac - 409

QY 121 gctgtcagctctgaagaggctgtctcttccttccttcacccaagaactggggaagccaac 180  
|| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 410 --tgcctcctccaagagaccagcccattcttcgacttcagaacttggggaagtcatac 467

QY 181 actactgactttgggttaactat 203  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 468 aacactgcctttgaattaatat 490

Search completed: June 21, 2002, 12:02:57  
Job time: 14920 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 06:14:52 ; Search time 2828.95 Seconds  
(without alignments)  
1016.226 Million cell updates/sec

Title: US-09-763-498-5  
Perfect score: 213  
Sequence: 1 gaagaggataatgattt.....ggtaactatgctgttttaa 213

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estio:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	58.7	479	9	AA030324 mi08c10.r
2	125	58.7	883	11	AK004061 Mus muscu
3	97.4	45.7	539	9	AW368430 CM3-HT019
4	97.4	45.7	555	9	AW361172 RCL-CT025
5	97.4	45.7	555	10	BE695960 RCL-CT025
6	97.4	45.7	557	9	AW368437 CM3-HT019
7	97.4	45.7	559	9	AW578451 RCL-CT025
8	95.8	45.0	436	9	AW361164 RCL-CT025
9	95.8	45.0	536	9	AW853610 RCL-CT025
10	93.8	44.0	434	9	AW753217 RCL-CT025
11	91	42.7	560	9	AW361245 RCL-CT025
12	65.8	30.9	870	10	BF244205 601863146
13	65.6	30.8	612	10	BM386666 UI-R-CN1-
14	62.6	29.4	393	9	AV011778 AV011778
15	56.6	26.6	1219	11	AK009787 Mus muscu
16	48.8	22.9	1051	11	AK009741 Mus muscu
17	48.8	22.9	1199	11	AK008977 Mus muscu

18	48.8	22.9	1531	11	AK010020
19	48.8	22.9	2843	11	AK014576
20	48.6	22.8	594	10	BI961215 MONO3_7_E
21	46.8	22.0	726	10	BI089828 602855071
22	46.8	22.0	858	10	BI090567 602855674
23	45.8	22.0	932	9	AL545100 AL545100
24	45.8	21.5	1020	10	BG245180 602357579
25	42.6	20.0	626	9	BB612586 BB612586
26	41.8	19.6	435	10	W78043 zdt2d01.r1
27	41.4	19.4	356	10	BE477245 160853 BA
28	41.4	19.4	508	9	AW464284 BP230015A
29	41.2	19.3	635	9	AW262191 xq62f01.x
30	41.2	19.3	889	9	AL540334 AL540334
31	41.2	19.3	910	9	AL549965 AL549965
32	41.2	19.3	938	10	BE563703 601335323
33	41.2	19.3	955	10	BM009048 603618892
34	41.2	19.3	997	9	AL554778 AL554778
35	41	19.2	531	9	AW951593 EST363663
36	39.6	18.6	371	10	BI020838 CM4-MT021
37	39.6	18.6	549	10	BE706905 QV0-HT036
38	39.6	18.6	640	10	BG288796 602388126
39	39.6	18.6	864	10	BI489807 603031536
40	38.8	18.2	281	10	R50241 yJ58a03.r1
41	38.6	18.1	260	10	R48871 yJ54F05.r1
42	38.6	18.1	350	10	BI020732 CM4-MT021
43	37.2	17.5	421	10	BI289899 UI-R-DK0-
44	34.6	16.2	970	9	BB622514 BB622514
45	34.2	16.1	458	9	AW636636 b149a05.w

#### ALIGNMENTS

RESULT 1

AA030324 479 bp mRNA linear EST 21-JAN-1997  
mi08c10.r1 Soares mouse placenta 4NbMPL3.5 14.5 Mus musculus cDNA  
clone IMAGE:459858 5', mRNA sequence.

AA030324.1 GI:1497479  
EST.  
house mouse.

Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)

Contact: Marra M/Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:276746

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 467.

Location/Qualifiers

1. 479

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:459858"

/clone\_lib="Soares mouse placenta 4NbMPL3.5 14.5"

/sex="unknown"

FEATURES

source

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/tissue_type="placenta"
/dev_stage="adul"
/ab_host="DH10B"
/Note="Organ: placenta; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'.
TGTTCACCAATCTGAAGTGGAGCGCGCGAAATTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 148 a 108 c 102 g 121 t
ORIGIN

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Best Local Similarity 74.2%; Pred.No. 3.2e-27;
Matches 158; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 1 gaaagagataatgattgtacacacccagcctgtgaagtccttctcttctac 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 204 GAAGGGAACATATGAATGTACAAACAAAGAAACCTGTAAAGCGCTCTCTCTAT 263
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 cacagcagagtgagggaactccaccctcgagctgtggttccctcggtggttcac 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 264 CACAAGAGAGTGGTACACCTCTACATTTGAGTCTGCAGCCTTCCCTGGTGGTTCATC 323
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 gctgtcagctctgaaggagctgtctctctcatctaccacgaactggggaagccaac 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 324 GCTGTCTGCTTAAGGGAGCTGCCCACTCATCTGACCAAGAACTGGGGAAATCTTC 383
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 actactgaacttgggttaactatgctgttttaa 213
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 384 ATCACTGCTCGAGATGATGTGGTACATTAA 416
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RESULT 2
LOCUS AK004061 883 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus 18 days embryo whole body cDNA, RIKEN full-length
(capsilon), full insert sequence.
ACCESSION AK004061.1 GI:12835089
VERSION HTC; CAP trapper.
KEYWORDS Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA,
SOURCE clone.lib:RIKEN full-length enriched mouse cDNA library
clone:1110033G16.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2 (sites)
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3 (sites)
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuaki,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED 11076861
4 (sites)
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 883)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Horii,F.,
Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Teijima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGAGAGAGCGCCGCACTCGAGTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to Not - 5.0. Second strand cDNA
was prepared with the primer adapter of sequence15'
GAGAGAGAGAGTCCCAAGAGCTCAATTTATTTAAATTAACCCCCCCCC 3']. cDNA was
cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
XhoI. Host: SOLR.
FEATURES
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="MGD:MGI:1900693"
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/clone="1110033G16"
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evidence:ISS
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ORIGIN				
Query Match	45.7%	Score 97.4;	DB 9;	Length 539;
Best Local Similarity	70.9%;	Pred. No. 7.2e-19;		
Matches 144;	Conservative 0;	Mismatches 56;	Indels 3;	Gaps 1;
QY	1	gaaagagataatgattgtacaaacacacacgagcctgtgaagtccttctctctac	60	
Db	497	GAGCAGAAATCATGGATCTCTGTGGCAACACCGAGCCGTGAACCCCTTCCTTTCTAC	438	
QY	61	cacagccagatggcagaaactccaccttcgagctgtggtcttccctggtggttcac	120	
Db	437	CGTGCCAGACTGGTAGACCTCCACCTTGAGTCTGTGGCCCTCCCGACTGGTTCAT-	377	
QY	121	gtgtcagctgaaggaggtgtctctctatcctatcccaagaactcgggaagcaaac	180	
Db	378	--TGCCCTCCACAGAGACGACGCCATCATTTCTGACTTTCAGAACTTGGAAGTCATAC	321	
QY	181	actactgacttgggttaactat	203	
Db	320	ACACTGCGCTTTGAATTAATAT	298	
RESULT	4			
LOCUS	AW3611172	555 bp	mrna	linear EST 04-FEB-2000
DEFINITION	RC1-CT0251-141099-012-h04	CT0251	Homo sapiens	cdna, mRNA sequence.
ACCESSION	AW3611172			
VERSION	AW3611172.1	GI:6865822		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 555)			
JOURNAL	HCGP <a href="http://www.ludwig.org.br/ORESTES">http://www.ludwig.org.br/ORESTES</a> .			
COMMENT	The FAPESP/LICR Human Cancer Genome Project Unpublished (1999) Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: <a href="mailto:asimpson@ludwig.org.br">asimpson@ludwig.org.br</a> This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL ( <a href="http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&amp;t2=RC1-CT0251-141099-012-h04&amp;t3=1999-10-14&amp;t4=1">http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&amp;t2=RC1-CT0251-141099-012-h04&amp;t3=1999-10-14&amp;t4=1</a> ) Seq primer: puc 18 forward High quality sequence stop: 555.			
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	/dev_stages="Adult"			
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BASE COUNT	148 a	129 c	130 g	147 t
ORIGIN				1 others
Query Match	45.7%	Score 97.4;	DB 9;	Length 555;
Best Local Similarity	70.9%;	Pred. No. 7.3e-19;		

[illegible]

Query Match	45.7%;	Score 97.4;	DB 10;	Length 555;
Best Local Similarity	70.9%;	Pred. No. 7.3e-19;		
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1	gaaagagataatgattgtatacaacacccgagcctgtgaagtcccttctctctac	60		
517	GAGCAGAAATCATGATCTGATGGCCAAACCGAGCCGTGAAACCTTCCTTTCTTAC	458		
61	cacagccagagtgagcaggaactcaccttcgagtcgtgtgcttccctggctgggttcac	120		
457	CGTGCCCAAGACTGTAGAGACTCCACCTTGAGCTGTGGCCTTCCCGACTGGTTTCAT-	397		
121	gctgtcagctctgaagaggctctctctctactcttaccacgaagaactggggaaacccaac	180		
398	--TGCCCTCCCAAGAGAGACACGAGCCCATCATCTGACTTCAGAACTTGGGAAGTCATAC	341		
181	actactgactttgggttaactat	203		
340	AACACTGCCTTTGAATTAATAT	318		

RESULT	6
LOCUS	AW368437/c
DEFINITION	CM3-RH0192-071099-022-h06 HT0192 Homo sapiens cDNA, linear mRNA EST 04-FEB-2000
ACCESSION	AW368437
VERSION	AW368437.1 GI:6873087
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 557)
AUTHORS	HCCP <a href="http://www.ludwig.org.br/ORESTES">http://www.ludwig.org.br/ORESTES</a> .
TITLE	The FAPESP/LICR Human Cancer Genome Project
JOURNAL	Unpublished (1999)
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Email: [asimpon@ludwig.org.br](mailto:asimpon@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 project. This entry can be seen in the following URL  
<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM3&t2=CM3-HT0192>  
 (071099-022-h06&t3=1999-10-07&t4=1)  
 Seq primer: puc.18 forward  
 High quality sequence start: 43  
 High quality sequence stop: 557.  
 Location/Qualifiers  
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FEATURES  
     source

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/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site.1: SmaI;
Site.2: SmaI; A mini-library was made by cloning products
derived from ORSTPS PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription o
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
149 a 130 c 130 g 147 t 1 others
BASE COUNT
ORIGIN
Query Match 45.7%; Score 97.4; DB 9; Length 557;
Best Local Similarity 70.9%; Pred. No. 7.3e-19;
Matches 144; Conservative 0; Mismatches 56; Indels 3; Gaps 1
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Db 515 GAGCAGAAATCATGATCTGTATGGCCAAACCGACCGCTGAAACCTTCTCTTCTAC 456
Qy 61 cacagcagagtgagcaggaactcaactctgagctgtggtcttccctggtggttcac 120
Db 455 CGTGCCAAAGACTGCTAGGACCTCCACCTTGAGCTGTGTGGCCCTCCCGGACTGGTTTCAT- 395
Qy 121 gctgtcagctctgaagagagctgtctctcctcctccttaccacaagaactggggaagccaac 180
Db 396 --TGCCTCCCTCCCAAGAGAGACACCGCCATCATTTGACTTCAGAACTTGGGAAGTCATAC 339
Qy 181 actactgactttgggttaactat 203
Db 338 AACACTGCCCTTGAATTAATAT 316

RESULT 7
AW578451/c
LOCUS RC1-CT0252-030100-023-b06 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW578451
VERSION AW578451.1 GI:7253500
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 559)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0252-
030100-023-b06&t3=2000-01-03&t4=1)
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 148 a 130 c 132 g 149 t
ORIGIN
Query Match 45.7%; Score 97.4; DB 9; Length 559;
Best Local Similarity 70.9%; Pred. No. 7.3e-19;
Matches 144; Conservative 0; Mismatches 56; Indels 3; Gaps 1;
Qy 1 gaaagagatataatgattgtacacacacccgagcctgtgaagctcttctcttctac 60
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Db 398 --TGCCTCCCTCCCAAGAGAGACACCGCCATCATTTGACTTCAGAACTTGGGAAGTCATAC 341
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Db 340 AACACTGCCCTTGAATTAATAT 318

RESULT 8
AW361164/c
LOCUS RC1-CT0251-141099-012-c02 CT0251 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW361164
VERSION AW361164.1 GI:6865814
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 436)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0251-
141099-012-c02&t3=1999-10-14&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 35
High quality sequence stop: 436.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0251"
/dev_stage="Adult"
/notes="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 123 a 96 c 103 g 114 t
ORIGIN
Query Match 45.0%; Score 95.8; DB 9; Length 436;
Best Local Similarity 70.4%; Pred. No. 2e-18;
Matches 143; Conservative 0; Mismatches 57; Indels 3; Gaps 1;
Qy 1 gaaagagatataatgattgtacacacacccgagcctgtgaagctcttctcttctac 60
Db 394 GAGCAGAAATCATGATCTGTATGGCCAAACCGACCGCTGAAACCTTCTCTTCTAC 335
Qy 61 cacagcagagtgagcaggaactccacctctgagctgtggtcttccctggtggttcac 120
Db 334 CGTGCCAAAGACTGGTAGGACCTCCACCTTGAGTCTGTGGCTTCCCGGACTGGTTTCAT- 274
Qy 121 gctgtcagctctgaagagagctgtctcctcctccttaccacaagaactggggaagccaac 180
Db 275 --TGCCTCCCTCCCAAGAGAGACACCGCCATCATTTGACTTCAGAACTTGGGAAGTCATAC 218

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[illegible][illegible]



Db 314 AACACTAATCTACTTAGATTCTGTGGAATAA 346

RESULT 13  
BM386666/c  
LOCUS  
DEFINITION UI-R-CNL1-cjg-1-09-0-UI.s1 UI-R-CNL1 Rattus norvegicus cDNA clone  
UI-R-CNL1-cjg-1-09-0-UI 3', mRNA sequence.

ACCESSION BM386666  
VERSION BM386666  
KEYWORDS BM386666.1 GI:18186719  
SOURCE EST.  
ORGANISM Norway rat.  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 612)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)

JOURNAL 9704477  
MEDLINE Contact: Soares, MB  
COMMENT Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: mscares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. The sequence tag present in the cDNA between the NotI site  
and the oligo-dT track served to identify it as a clone from the  
normalized fundus library cDNA library Preparation: M.B. Soares Lab.  
Clone distribution: clones will be available through Research  
Genetics (www.resgen.com)  
Seq primer: M13 Forward  
POLYA=Yes.

FEATURES  
source  
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/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pRT3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-CNL1  
library is a subtracted library derived from the following  
pool of seven normalized rat libraries: normalized rat  
seminal vesicles, normalized rat penis, normalized rat  
bladder, normalized rat cervix, normalized rat brown  
adipose, normalized rat fundus, and normalized rat  
salivary gland. It was constructed according to the  
procedure described by Bonaldo, Lennon & Soares (Genome  
Research Genome 6: 791-806, 1996). For construction of  
the CNL1 library, plasmid DNA from the pool of normalized  
libraries was electroporated into competent bacteria for  
the production of single-stranded circular DNA. This was  
then used as a tracer in a subtractive hybridization with  
a driver (PCR amplified inserts from a plamid DNA template  
preparation) comprising: a) a pool of about 34,000 clones  
from the Rat Unigene Set corresponding to plates R-5-AA-NN  
excluding plates R-5-MM and MN. This pool represented 40%  
of the final driver population. b) a pool of about 29,000  
clones from subtracted libraries CA0 and CAL corresponding  
to plates R-CA0-AWV through R-CA0-BHY, R-CA0-AXZ through  
R-CA0-BAZ, R-CA0-BFE through R-CA0-BKJ-K, R-CA0-BKJ-K,  
R-CA0-BKE, R-CA0-BKG-H, R-CA0-BKJ-K, R-CA0-BKP through  
R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA,  
R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through

R-CA0-BOJ, R-CA0-BPA through R-CA0-BPG, R-CA1-BBA through  
R-CA1-BDA, R-CA1-BHZ through R-CA1-BKB, R-CA1-BKD, R-CA1-BKF,  
R-CA1-BJT through R-CA1-BKE, R-CA1-BLF, R-CA1-BLH through  
R-CA1-BKI, R-CA1-BKT, R-CA1-BLJ, R-CA1-BLV, R-CA1-BNR, and  
R-CA1-BLE. The resulting pool represented 20% of the  
final driver population. c) a pool of about 15,000 clones  
from non-normalized libraries CS0s, CT0s, CU0s, CW0s, CX0s  
and normalized libraries CS0, CT0, CU0, CW0, and CX0  
corresponding to plates R-CS0s-CBD through R-CS0s-CBO,  
R-CT0s-CAM through R-CT0s-CAX, R-CU0s-CBP through  
R-CU0s-CCA, R-CW0s-CCB through R-CW0s-CCM, R-CX0s-CCN  
through R-CX0s-CCX, R-CS0-BSD, R-CS0-BTD through R-CS0-BTV  
, R-CS0-BVM, R-CT0-BTW through R-CT0-BUP, R-CU0-BVN,  
R-CU0-BUQ through R-CU0-BVL, R-CW0-BVY through R-CW0-BWP,  
R-CW0-BXN through R-CW0-BXO, R-CX0-BWQ through R-CX0-BXM.  
The resulting pool represented 5% of the final driver  
population. d) a pool of about 5,000 clones (1,000 from  
non-normalized eye library CV0 and 4,000 from normalized  
eye library CV1) corresponding to plates R-CV0-BRH through  
R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through  
R-CV1-BTC, and R-CV1-BVO through R-CV1-BVU. This pool  
represented about 5% of the final driver population. e) A  
pool of about 10,000 clones from subtracted library BS2,  
BV0 and BV0p (7-9.5 kb cDNA library fraction from rat  
whole embryo), and BX0 (0.5-7kb cDNA library fraction from  
rat whole embryo) corresponding to plates R-BS2-BDB  
through R-BS2-BFB, R-BV0-ANK through R-BV0-ANR, R-BV0p-AOI  
through R-BV0p-AOX, and R-BX0-AQY through R-BX0-ASH. The  
resulting pool represented 5% of the final driver  
population. f) a pool of about 7,000 clones from the  
seven non-normalized libraries that make up the tracer  
including CV0, CZ0, DA0, DB0, DD0, and DE0  
corresponding to plates R-CY0-BXP through R-CY0-BXZ,  
R-CZ0-BYA through R-CZ0-BYI, R-CZ0-BZB-C, R-DA0-BYJ  
through R-DA0-BYP, R-DA0-BZD through R-DA0-BZH, R-DB0-BYQ  
through R-DB0-BZA, R-DC0-BZI through R-DC0-BZQ, R-DC0-CAY  
through R-DC0-CBA, R-DD0-BZR through R-DD0-CAA,  
R-DD0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The  
resulting pool represented about 10% of the final driver  
population. g) a pool of about 2,000 clones from the pool  
of normalized libraries, CN0, that makes up the tracer.  
The corresponding plates are R-CN0-BKW through R-CN0-BLD,  
R-CN0-BLG, R-CN0-BLP through R-CN0-BLR, R-CN0-BLT,  
R-CN0-BLM-X, R-CN0-BMB, and R-CN0-BMF through R-CN0-BML.  
This pool represented 5% of the final driver population.  
h) a pool of the 28 most abundant clones in the CN0 pool  
corresponding to the following addresses: bkx-a-09-0-UI,  
bkx-b-09-0-UI, bkx-b-11-0-UI, bkx-b-10-0-UI, bkx-d-01-0-UI  
, bkx-d-06-0-UI, bkx-g-08-0-UI, bkx-h-12-0-UI,  
bkx-a-05-0-UI, bkz-a-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI  
, bkz-c-09-0-UI, bkz-d-10-0-UI, bla-a-01-0-UI,  
bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI  
, blb-a-12-0-UI, blb-f-02-0-UI, blc-a-11-0-UI,  
blc-e-95-0-UI, bld-1-08-0-UI, bld-f-02-0-UI, blg-h-04-0-UI  
, blr-a-05-0-UI, blt-f-08-0-UI. This pool represented 5%  
of the final driver population. i) One abundant CN0 clone  
(corresponding to the address bkz-a-11-0-UI) was digested  
with Not I and Eco RI and the resulting insert was gel  
purified. This purified insert was added directly to the  
driver so that it represented 5% of the final driver  
population.  
TAG\_LJB-UI-R-CNL1  
TAG\_TISSUE-fundus  
TAG\_SEQ=ITCGG+

BASE COUNT 160 a 130 c 124 g 198 t  
ORIGIN

Query Match 30.8%; Score 65.6; DB 10; Length 612;  
Best Local Similarity 58.9%; Pred. No. 3e-09;  
Matches 113; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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QY 7 gataaatggtattgtataaaccacccagcgtgtgaagtcctttctcttcttaccacagc 66
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Db 397 GACATCATGATTTGTACATGAGAAAAAGACACAGAACCCCTTCTCTCTACCATGGC 338
QY 67 cagagtgcagggaactccacttcagctgtgtgtgttccctgcgtgttcctcgtctc 126
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Db 337 ATAGAGGGATCTACTTGTCTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 278
QY 127 agctctgaagagcgtctctctcctccttaccacgaactagggaagcccaactact 186
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Db 277 TCTTCCACAGCAGACAAACATCTCTTACACAGAGAGGGGCTGAAGCTAATACACT 218
QY 187 gactttgggtta 198
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Db 217 AACTTCTACTTA 206

RESULT 14
AV011778
LOCUS
DEFINITION
AV011778 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA
clone 1110033G16, mRNA sequence.
ACCESSION
AV011778
VERSION
AV011778.1 GI:4788765
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 393)
AUTHORS
Carninci,P., Shibata,K., Okawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
Kikuchi,N., Kojima,Y., Matsuyama,T., Niihuma,H., Oda,H., Owa,C.,
Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tomioka,N.,
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
RIKEN Mouse ESTs
TITLE
RIKEN Mouse ESTs
JOURNAL
Unpublished (1999)
COMMENT
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
location/Qualifiers
1..393
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QY 73 ggcaggaaactccacttcagctgtgtgttccctgcgtgttcctcgtgttcagctctc 132
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Db 14 GACATAACCTCAACATTTAATTCTTACAGCCCTTCTATAGATGGTTTCATCGCTATTTCTAT 73
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Db 74 AATGGGAGCTGCCACACATTTTGGACCCAAAGAACTGGGGGAAATCTTCATCATCAGCTTC 133
QY 193 gggtaactatcgtgtgttttaa 213
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Db 134 GAGATGATTGTGGAACATTAA 154

RESULT 15
AK009787
LOCUS
DEFINITION
AK009787 1219 bp mRNA linear HTC 19-JAN-2002
Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310043N20:homolog to FILL ETA, full insert
sequence.
ACCESSION
AK009787
VERSION
AK009787.1 GI:12844799
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
clone.lib:RIKEN full-length enriched mouse cDNA library
clone:2310043N20.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
REFERENCE
Carninci,P. and Hayashizaki,Y.
AUTHORS
Carninci,P. and Hayashizaki,Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
2 (sites)
REFERENCE
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
AUTHORS
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159
3 (sites)
REFERENCE
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
AUTHORS
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PUBMED
11076861
4 (sites)
REFERENCE
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNAL
Nature 409, 685-690 (2001)
MEDLINE
11076861
5 (bases 1 to 1219)
REFERENCE
Adechi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,K., Sakai,K., Sano,H., Sasaki,D.,
Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Tejima,Y., Toyota,T., Yamamura,T., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.

```

TITLE Direct Submission  
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel.81-45-503-9222, Fax:81-45-503-9216]  
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

Search completed: June 21, 2002, 11:09:00  
Job time: 17648 sec

cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cdna was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cdna was prepared by using thermostable thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cdna went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cdna was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTCGAGTTAATTAATATCCCCCCCCCC 3']. cdna was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.  
Host: SOLR.

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Query Match 26.6%; Score 56.6; DB 11; Length 1219;  
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Matches 107; Conservative 0; Mismatches 84; Indels 0; Gaps 0;  
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QY 61 cacagcagagtgaggagaaacccaccttcgagctgtggcttccctggctgttcac 120  
DB 477 CATGGCATAGAGGGCTCCACTTCTGTCTTTTCAGTCAGTCCTCTATCCTGGCTTTATA 536  
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DB 537 GCCACTCTTCATAGAAAGACAGACAATCATCCTCACATCAGCGGGTAAATTTGGTT 596  
QY 181 actactgactt 191  
DB 597 AACACTAACTT 607





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:01:09 ; Search time 73.84 Seconds  
(without alignments)  
105.297 Million cell updates/sec

Title: US-09-763-498-6

Perfect score: 371

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT.\*  
9: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT.\*  
10: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT.\*  
11: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT.\*  
12: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT.\*  
13: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT.\*  
14: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT.\*  
15: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT.\*  
16: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT.\*  
17: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT.\*  
18: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT.\*  
19: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT.\*  
20: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT.\*  
21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	371	100.0	70	AAV70216	Partial human Interleukin-1
2	371	100.0	158	AAV70217	Human Interleukin-1
3	371	100.0	158	AAV70218	Human Interleukin-1
4	371	100.0	273	AAE03417	Human Interleukin-1
5	309	83.3	130	AAE03417	Human Interleukin-1
6	238	64.2	72	AAE03417	Human Interleukin-1
7	238	64.2	98	AAE03417	Human Interleukin-1
8	238	64.2	157	AAE03417	Human Interleukin-1
9	238	64.2	160	AAE03417	Human Interleukin-1
10	238	64.2	160	AAE03417	Human Interleukin-1
11	208.5	56.2	134	AAE03417	A novel polypeptid

12	208.5	56.2	134	21	AAV96935	Human IL-1 recepto
13	208.5	56.2	169	19	AAW63136	Interleukin-1 rece
14	208.5	56.2	169	20	AAV24043	A human SPOIL-1 pr
15	208.5	56.2	169	20	AAV24395	Human interleukin-
16	208.5	56.2	169	22	AAE06656	Human interleukin-
17	208.5	56.2	169	22	AAE06656	Human interleukin-
18	208.5	56.2	173	22	AAE06656	Human IL-1ra prote
19	208.5	56.2	173	22	AAU16937	Human novel secret
20	208.5	56.2	208	20	AAV24044	A human SPOIL-II p
21	201.5	54.3	172	22	AAU17010	Human novel secret
22	201.5	54.3	172	22	AAE09702	Human gene 13 enco
23	184	49.6	157	22	AAE04299	Human Interleukin-
24	184	49.6	170	22	AAE04299	Human IL-1 eta. H
25	147	39.6	68	20	AAE05000	Human interleukin-
26	127	34.2	154	22	AAE06663	SPOIL protein cons
27	127	34.2	155	21	AAE06663	Mouse interleukin-
28	127	34.2	155	21	AAE06663	Murine IL-1 recept
29	127	34.2	155	22	AAE06663	Murine IL-1. Mu
30	127	34.2	155	22	AAE06663	Invention related
31	127	34.2	156	19	AAE06663	Murine interleukin
32	127	34.2	156	20	AAE06663	Rodent interleukin
33	127	34.2	156	21	AAE06663	Mouse interleukin
34	127	34.2	156	21	AAE06663	Murine IL-1 homolo
35	125	33.7	258	22	AAE06663	Murine TANGO-93 pr
36	124	33.4	80	20	AAE06663	Novel human diagno
37	124	33.4	80	20	AAE06663	A human interleuki
38	124	33.4	154	22	AAE06663	Protein encoded by
39	124	33.4	154	22	AAE06663	Interleukin-1. re
40	124	33.4	155	20	AAE06663	Human interleukin
41	124	33.4	155	21	AAE06663	Human IL-1 recepto
42	124	33.4	155	21	AAE06663	Human IL-1 homolo
43	124	33.4	155	21	AAE06663	Human IL-1 homolo
44	124	33.4	155	21	AAE06663	Human TANGO-93 pr
45	124	33.4	155	22	AAE06663	Human interleukin-
			155	22	AAE06663	Human PRO4342. Ho

## ALIGNMENTS

RESULT 1

AAV70216  
ID AAV70216 standard; Protein; 70 AA.

AC AAV70216;

DT 06-JUN-2000 (first entry)

Partial human Interleukin-1 epsilon protein.

DE Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;  
KW gene mapping; immune system; treatment; inflammatory disease;  
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
KW psoriasis; human.

OS Homo sapiens.

PN WO200011174-A1.

PD 02-MAR-2000.

PF 20-AUG-1999; 99WO-US18771.

PR 21-AUG-1998; 98US-0097413.

PR 31-AUG-1998; 98US-0098595.

PR 11-SEP-1998; 98US-0099974.

PA (IMMV ) IMMUNEX CORP.

PI Sims JE, Smith DE;

XX WPI; 2000-237653/20.

XX N-PSDB; AA251246.

DR

DR

XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
PT treat inflammatory and immune system-related diseases such as  
PT rheumatoid arthritis and inflammatory bowel disease -  
XX  
PS Claim 1b; Fig 2; 76pp; English.  
XX  
CC The present sequence is the partial Interleukin-1 (IL-1) epsilon  
CC protein encoded by the 3' exon of IL-1 epsilon DNA. IL-1 epsilon  
CC gene is mapped to chromosome 2q and is mainly expressed in spleen,  
CC lymph node, thymus, tonsil and leucocyte tissues. IL-1 epsilon is  
CC a cytokine, with antiinflammatory, immunosuppressant,  
CC antirheumatic, antiarthritic and antipsoriatic activity. The DNA  
CC sequence can be used in chromosome identification, gene mapping and  
CC study of immune system. IL-1 epsilon can be used in the treatment of  
CC inflammatory or autoimmune diseases such as rheumatoid arthritis,  
CC inflammatory bowel disease and psoriasis.  
XX  
SQ Sequence 70 AA;  
Query Match 100.0%; Score 371; DB 21; Length 70;  
Best Local Similarity 100.0%; Pred. No. 7.2e-38;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EKDIMLYNQPEPVKSFYHSQSGRNSTFESVAFPGWFIASVSEGCPILITQELGKAN 60  
DB 1 ekdimlynpvpkvsflfhsqsgnrnstfesvafpgwfiavsegcpililtqelgkan 60  
QY 61 TTDFGLTMLF 70  
DB 61 ttdfgltmlf 70  
RESULT 2  
AAAY70217  
ID AAY70217 standard; Protein; 158 AA.  
XX  
AC AAY70217;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE Human Interleukin-1 epsilon protein.  
XX  
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;  
KW gene mapping; immune system; treatment; inflammatory disease;  
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
KW psoriasis; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200011174-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-US18771.  
XX  
PR 21-AUG-1998; 98US-0097413.  
XX  
PR 31-AUG-1998; 98US-0098595.  
XX  
PR 11-SEP-1998; 98US-0099974.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Sims JE, Smith DE;  
XX  
XX WPI: 2000-237653/20.  
DR N-PSDB; AAZ51247.  
XX  
XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
PT treat inflammatory and immune system-related diseases such as  
PT rheumatoid arthritis and inflammatory bowel disease -  
XX

PS Claim 1b; Fig 2; 76pp; English.  
XX  
CC The present sequence is that of human Interleukin-1 (IL-1) epsilon  
CC protein. IL-1 epsilon gene is mapped to chromosome 2q and is mainly  
CC expressed in spleen, lymph node, thymus, tonsil and leucocyte  
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,  
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic  
CC activity. It can be used in the treatment of inflammatory or autoimmune  
CC diseases such as rheumatoid arthritis, inflammatory bowel disease and  
CC psoriasis. The DNA sequence can be used in chromosome identification,  
CC gene mapping and study of immune system.  
XX  
SQ Sequence 158 AA;  
Query Match 100.0%; Score 371; DB 21; Length 158;  
Best Local Similarity 100.0%; Pred. No. 1.8e-37;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EKDIMLYNQPEPVKSFYHSQSGRNSTFESVAFPGWFIASVSEGCPILITQELGKAN 60  
DB 89 ekdimlynpvpkvsflfhsqsgnrnstfesvafpgwfiavsegcpililtqelgkan 148  
QY 61 TTDFGLTMLF 70  
DB 149 ttdfgltmlf 158  
RESULT 3  
AAAY70218  
ID AAY70218 standard; Protein; 158 AA.  
XX  
AC AAY70218;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE Human Interleukin-1 epsilon polymorphic variant.  
XX  
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;  
KW gene mapping; immune system; treatment; inflammatory disease;  
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
KW psoriasis; polymorphic variant; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200011174-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-US18771.  
XX  
PR 21-AUG-1998; 98US-0097413.  
XX  
PR 31-AUG-1998; 98US-0098595.  
XX  
PR 11-SEP-1998; 98US-0099974.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Sims JE, Smith DE;  
XX  
XX WPI: 2000-237653/20.  
DR N-PSDB; AAZ51248.  
XX  
XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
PT treat inflammatory and immune system-related diseases such as  
PT rheumatoid arthritis and inflammatory bowel disease -  
XX  
PS Claim 1b; Fig 2; 76pp; English.  
XX

CC The present protein sequence is that of human Interleukin-1 (IL-1)  
 CC epsilon polymorphic variant. IL-1 epsilon gene is mapped to chromosome 2q  
 CC and is mainly expressed in spleen, lymph node, thymus, tonsil and  
 CC leucocyte tissues. IL-1 epsilon is a cytokine, with antiinflammatory,  
 CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic  
 CC activity. It can be used in the treatment of inflammatory or autoimmune  
 CC diseases such as rheumatoid arthritis, inflammatory bowel disease and  
 CC psoriasis. The DNA sequence can be used in chromosome identification,  
 CC gene mapping and study of immune system.

XX Sequence 158 AA;

Query Match 100.0%; Score 371; DB 21; Length 158;

Best Local Similarity 100.0%; Pred. No. 1.8e-37;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKDIMLYNQPEPVKSLFLYHSQSGRNSTFESVAFPGWFIASVSGGCPILITQELGKAN 60

Db 89 ekdimlyngpepvksflfysqsgsrnstfesvaipgwfiasvsggcpililtqelgkan 148

OY 61 TTDFGLTMLF 70

Db 149 ttdfgltmlf 158

RESULT 4

AAE03417  
 ID AAE03417 standard; Protein; 273 AA.

XX AC AAE03417;

DT 03-AUG-2001 (first entry)

DE Human interleukin-1 receptor antagonist-like (IL-lra-L).

XX Human; interleukin-1 receptor antagonist-like protein; IL-lra-L; therapy;  
 KW rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;  
 KW joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;  
 KW transplant rejection; graft versus host disease; strain; sprain; leprosy;  
 KW cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;  
 KW clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;  
 KW myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;  
 KW acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;  
 KW eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;  
 KW hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;  
 KW infertility; endometriosis; retinal neuropathy; acute pancreatitis;  
 KW Kawasaki's disease; cancer.

XX Homo sapiens.

OS WO200141792-A1.

PN 14-JUN-2001.

PD 04-DEC-2000; 2000WO-US32891.

PF 10-DEC-1999; 99US-0170105.

PR 28-NOV-2000; 2000US-0724859.

XX (AMGE-) AMGEN INC.

PI Calzone FJ, Luethy R, Boedigheimer MJ, Zhu J, Chung Y, Jing S;

XX WPI; 2001-381495/40.

DR N-PSDB; AAD06911.

XX Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the  
 PT polypeptide encoded by the nucleic acid is useful diagnosis, treatment,  
 PT and prevention of diseases such as arthritis, diabetes, transplant  
 PT rejection

PS Claim 13; Fig 1A; 127pp; English.

XX The present sequence is human interleukin-1 receptor antagonist-like  
 CC (IL-lra-L) protein. IL-lra-L is useful for treating, preventing or  
 CC ameliorating IL-lra-L polypeptide-related disease, condition or disorder  
 CC which include rheumatoid arthritis, psoriatic arthritis, inflammatory  
 CC arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,  
 CC lupus, diabetes, transplant rejection, inflammatory joint disease, graft  
 CC versus host disease and inflammatory conditions resulting from strain,  
 CC sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human  
 CC immunodeficiency virus (HIV) infection, clostridium-associated  
 CC diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,  
 CC anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory  
 CC disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,  
 CC psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,  
 CC Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,  
 CC lymphomas, lung and breast cancer, leukaemias, infertility,  
 CC endometriosis, retinal degeneration, retinal neuropathy, acute  
 CC pancreatitis and Kawasaki's disease.

XX Sequence 273 AA;

Query Match 100.0%; Score 371; DB 22; Length 273;

Best Local Similarity 100.0%; Pred. No. 3.4e-37;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKDIMLYNQPEPVKSLFLYHSQSGRNSTFESVAFPGWFIASVSGGCPILITQELGKAN 60

Db 204 ekdimlyngpepvksflfysqsgsrnstfesvaipgwfiasvsggcpililtqelgkan 263

OY 61 TTDFGLTMLF 70

Db 264 ttdfgltmlf 273

RESULT 5

AAE85001

ID AAE85001 standard; Protein; 130 AA.

XX AC AAE85001;

DT 06-AUG-2001 (first entry)

DE Human interleukin-1 receptor antagonist (NOVINTRA C) polypeptide.

XX NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;  
 KW gonadotropin-like protein; NOVGOIN; interleukin-1; NOVINTRA; human;  
 KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;  
 KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;  
 KW antiasthmatic; antiallergic.

XX Homo sapiens.

OS WO200140291-A2.

PN 07-JUN-2001.

PD 06-DEC-2000; 2000WO-US33029.

PR 06-DEC-1999; 99US-0169056.

PR 09-DEC-1999; 99US-0169866.

PR 09-DEC-1999; 99US-0169886.

PR 10-DEC-1999; 99US-0170252.

PR 12-JAN-2000; 2000US-0175740.

PR 05-DEC-2000; 2000US-0170252.

XX (CURA-) CURAGEN CORP.

XX Burgess CE, Prayaga SK, Shinkets RA, Rastelli L, Zerhusen BD;

PI Mezes PS;

XX WPI; 2001-374790/39.

DR N-PSDB; AAF83870.

XX Novel isolated human transmembrane, neuromedin peptide  
 PT gonadotropin-like protein and interleukin-1 receptor antagonist  
 PT proteins, useful for treating cancer, immune response disorder,  
 PT metabolic function disorders  
 XX  
 PS Claim 53; Fig 15B; 138pp; English.  
 XX  
 CC The invention provides novel polypeptides (NOVX) selected from human  
 CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),  
 CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor  
 CC antagonist proteins (NOVINTRA A and B). The invention also provides  
 CC methods in which a NOVX polypeptide, polynucleotide and antibody are  
 CC used in the detection, prevention and treatment of a broad range of  
 CC pathological states. NOVTRAN can be used to treat is a cell signaling  
 CC disorder such as cancer, immune response disorder, hematopoietic  
 CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat  
 CC endocrine disorder, muscle disorder, neurologic disorder, cancers of  
 CC central nervous system, breast, colon, ovary, kidney, prostate and  
 CC thyroid. NOVGON can be used to treat reproductive development disorder,  
 CC metabolic function disorder and melanoma. NOVINTRA A and B can be used  
 CC to treat bone metabolism or structure disorder, inflammatory response  
 CC disorder, immune regulation disorder, septic shock, stroke, diabetes,  
 CC arthritis and cancer. The present sequence represents the NOVINTRA C  
 CC polypeptide.  
 XX  
 SQ Sequence 130 AA;

Query Match 83.3%; Score 309; DB 22; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-30;  
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKDIMLYNOPEPVKSFIFYHSQSRNSTFESVAFPGWFIASVSGGCPILITQLGK 58  
 DB 73 ekdimlynpkpvksfifyhsqsrnstfesvafpgwfiavsggcpililtqlgk 130

RESULT 6  
 ID AAW86285  
 AC AAW86285;  
 XX  
 DT 19-FEB-1999 (first entry)  
 DE Rodent interleukin (IL)-1 epsilon partial polypeptide.  
 KW Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;  
 KW inflammatory response; immune system; diagnosis; agonist; antagonist;  
 KW chemokine.  
 XX  
 OS Mus sp.  
 PN WO9847921-A1.  
 XX  
 PD 29-OCT-1998.  
 XX  
 PF 17-APR-1998; 98WO-US06879.  
 XX  
 PR 06-AUG-1997; 97US-005111.  
 PR 21-APR-1997; 97US-0837627.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Bazan JF, Hedrick JA, Kastelein RA, Sana TR;  
 XX WPI: 1998-609976/51.  
 DR N-PSDB; AAV71959.  
 XX  
 PT Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.  
 PT regulating the immune system and inflammatory responses  
 XX

PS Disclosure; Page 91; 113pp; English.  
 XX  
 CC This represents a partial amino acid sequence of a rodent interleukin  
 CC (IL)-1 epsilon polypeptide. The invention relates to a recombinant  
 CC polypeptide that specifically binds polyclonal antibodies (Abs)  
 CC generated against a 12 consecutive amino acid segment of IL-1 delta  
 CC or IL-1 epsilon. Agonists or antagonists of these IL polypeptides are  
 CC used to regulate a cell involved in an inflammatory response. The IL-1  
 CC delta or IL-1 epsilon polypeptides and peptides are used to produce Abs  
 CC and antigen-Abs complexes. The polypeptides, Abs and the corresponding  
 CC nucleic acids regulate development and/or the immune system, and can be  
 CC used to diagnose and treat conditions associated with abnormal expression  
 CC of IL. Agonists or antagonists of IL-1 delta or IL-1 epsilon polypeptides  
 CC are used with agonists or antagonists of IL-1 alpha, IL-1 beta,  
 CC IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1 epsilon  
 CC polypeptides may be used as a soluble polypeptide or as a fusion protein  
 CC with another cytokine or chemokine.  
 XX  
 SQ Sequence 72 AA;

Query Match 64.2%; Score 238; DB 19; Length 72;  
 Best Local Similarity 63.8%; Pred. No. 1.3e-21;  
 Matches 44; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 EKDIMLYNOPEPVKSFIFYHSQSRNSTFESVAFPGWFIASVSGGCPILITQLGKAN 60  
 DB 3 egnimemynkpepvksfifyhsksgtstfesvafpgwfiavsggcpililtqlgeif 62

QY 61 TDFGLTML 69  
 DB 63 itdfemivv 71  
 RESULT 7  
 ID AAY24040  
 AC AAY24040;  
 XX  
 DT 30-SEP-1999 (first entry)  
 DE Amino acid sequence of a murine SPOIL-I protein.  
 XX  
 KW SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;  
 KW bone metabolism disorder; proinflammatory disorder; immune disorder;  
 KW inflammatory disease; septic shock; stroke; diabetes; arthritis;  
 KW intercolitis; pneumonitis; epithelial cell; skin disease;  
 KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;  
 KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;  
 KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;  
 KW osteogenesis imperfecta; fibrous dysplasia; hypophosphatasia;  
 KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;  
 KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;  
 KW bone fracture; ss.  
 XX  
 OS Mus sp.  
 PN WO9937662-A1.  
 XX  
 PD 29-JUL-1999.  
 XX  
 PF 26-JAN-1999; 99WO-US01575.  
 XX  
 PR 27-JAN-1998; 98US-0013810.  
 XX  
 PI (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 XX Busfield SJ;  
 XX WPI: 1999-458675/38.  
 DR N-PSDB; AAX86455.  
 XX



DR WPI: 1998-609976/51.  
 DR N-PSDB; AAV1960.  
 XX Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.  
 PT regulating the immune system and inflammatory responses  
 XX  
 XX Claim 1; Pages 92-93; 113pp; English.  
 XX  
 CC This represents a rodent interleukin (IL)-1 epsilon polypeptide. The  
 CC invention relates to a recombinant polypeptide that specifically binds  
 CC polyclonal antibodies (Abs) generated against a 12 consecutive amino acid  
 CC segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these  
 CC IL polypeptides are used to regulate a cell involved in an inflammatory  
 CC response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are  
 CC used to produce Abs and antigen-Abs complexes. The polypeptides, Abs and  
 CC the corresponding nucleic acids regulate development and/or the immune  
 CC system, and can be used to diagnose and treat conditions associated with  
 CC abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1  
 CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,  
 CC IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1  
 CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion  
 CC protein with another cytokine or chemokine.  
 XX  
 SQ Sequence 160 AA;  
 Query Match 64.2%; Score 238; DB 19; Length 160;  
 Best Local Similarity 63.8%; Pred. No. 3.2e-21;  
 Matches 44; Conservative 11; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 EKDIMLYNQPEPVKSLFYHQSQRNSTFESVAFPGWFIAYSSGCGPLILTQELGKAN 60  
 Db 91 egnimemynkpepkaslfyhhksgtstfesaafpgwfiavcskgscliltqelgeif 150  
 QY 61 TTDFGLTML 69  
 Db 151 itdfemiv 159  
 RESULT 10  
 AAY24049  
 ID AAY24049 standard; Protein; 160 AA.  
 XX  
 XX AAY24049;  
 XX  
 XX 30-SEP-1999 (first entry)  
 XX  
 DE Amino acid sequence of a murine SPOIL-II protein.  
 KW SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;  
 KW bone metabolism disorder; proinflammatory disorder; immune disorder;  
 KW inflammatory disease; septic shock; stroke; diabetes; arthritis;  
 KW intercolitis; pneumonitis; epithelial cell; skin disease;  
 KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;  
 KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;  
 KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;  
 KW osteogenesis imperfecta; fibrous dysplasia; hypophosphatasia;  
 KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;  
 KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;  
 KW bone fracture.  
 XX  
 OS Mus sp.  
 PN W09937662-A1.  
 XX  
 PD 29-JUL-1999.  
 XX  
 PF 26-JAN-1999; 98WO-US01575.  
 XX  
 PR 27-JAN-1998; 98US-0013810.  
 XX  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 XX

PI Busfield SJ;  
 XX  
 DR WPI: 1999-458675/38.  
 DR N-PSDB; AAX86460.  
 XX  
 PT New isolated SPOIL proteins, used to develop products for treating,  
 PT e.g. inflammatory and immune disorders  
 XX  
 XX Claim 8; Fig 6; 126pp; English.  
 PS  
 CC The present sequence represents a SPOIL-II protein. SPOIL proteins have  
 CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.  
 CC The SPOIL proteins are used as modulating agents in regulating a variety  
 CC of cellular processes. The products can be used for treating disorders  
 CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone  
 CC metabolism disorder, a proinflammatory disorder or an immune disorder.  
 CC They can be used for treating e.g. inflammatory diseases and disorders  
 CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,  
 CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and  
 CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma  
 CC and Kaposi's sarcoma and other epithelial cancers including squamous cell  
 CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and  
 CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's  
 CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,  
 CC fibrous dysplasia, hypophosphatasia, bone sarcoma, myeloma bone disorder  
 CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and  
 CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in  
 CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.  
 CC decrease bone fragility); and prevention and/or treatment of bone pain,  
 CC bone deformities and/or bone fractures. The products can also be used for  
 CC detection, diagnosis and screening assays.  
 XX  
 SQ Sequence 160 AA;  
 Query Match 64.2%; Score 238; DB 20; Length 160;  
 Best Local Similarity 63.8%; Pred. No. 3.2e-21;  
 Matches 44; Conservative 11; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 EKDIMLYNQPEPVKSLFYHQSQRNSTFESVAFPGWFIAYSSGCGPLILTQELGKAN 60  
 Db 91 egnimemynkpepkaslfyhhksgtstfesaafpgwfiavcskgscliltqelgeif 150  
 QY 61 TTDFGLTML 69  
 Db 151 itdfemiv 159  
 RESULT 11  
 AAB18924  
 ID AAB18924 standard; Protein; 134 AA.  
 XX  
 XX AAB18924;  
 XX  
 XX 08-FEB-2001 (first entry)  
 XX  
 DE A novel polypeptide designated PRO5737.  
 KW Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;  
 KW PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;  
 KW PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;  
 KW PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;  
 KW insulinemia; kidney disorder; Bergers disease; nephropathy;  
 KW Schonlein-Henoch purpura; celliac disease; dermatitis herpetiformis;  
 KW Crohns disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..17 /note= "signal sequence"  
 FT Modified-site 10..16 /note= "N-myristoylation site"  
 FT

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XX PN WO200056889-A2.
XX PD 28-SEP-2000.
XX PF 01-MAR-2000; 2000WO-US05601.
XX PR 23-MAR-1999; 99US-0125774.
XX PR 23-MAR-1999; 99US-0125778.
XX PR 24-MAR-1999; 99US-0125826.
XX PR 31-MAR-1999; 99US-0127035.
XX PR 05-APR-1999; 99US-0127706.
XX PR 21-APR-1999; 99US-0130359.
XX PR 27-APR-1999; 99US-0131270.
XX PR 27-APR-1999; 99US-0131272.
XX PR 27-APR-1999; 99US-0131291.
XX PR 04-MAY-1999; 99US-0132371.
XX PR 04-MAY-1999; 99US-0132379.
XX PR 04-MAY-1999; 99US-0132383.
XX PR 25-MAY-1999; 99US-0132383.
XX PR 08-JUN-1999; 99US-0135750.
XX PR 08-JUN-1999; 99US-0138166.
XX PR 20-JUL-1999; 99US-0144791.
XX PR 03-AUG-1999; 99US-0146970.
XX PR 09-DEC-1999; 99US-0170262.
XX PA (GETH ) GENENTECH INC.
XX PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
XX PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX DR WPI; 2000-628263/60.
XX DR N-PSDB; AAA96351.
XX PT Novel secreted and transmembrane polypeptides useful for diagnosing
XX PT tumour in a mammal, for identifying agonists and antagonists of the
XX PT polypeptide and for therapeutic use
XX PS Claim 12; Fig 32; 222pp; English.
XX CC The present sequence represents a secreted or transmembrane polypeptide.
XX CC The specification describes polypeptides designated PRO1484, PRO4334,
XX CC PRO1182, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
XX CC PRO4356, PRO4380, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
XX CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
XX CC useful for diagnosing tumour in a mammal. The polypeptides, their
XX CC agonists and antagonists are useful treating a condition associated with
XX CC expression or activity of the polypeptide. Conditions treated include
XX CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
XX CC capable of inducing proliferation of mammalian kidney mesangial cells
XX CC and are therefore useful for treating kidney disorders associated with
XX CC decreased mesangial cell function such as Bergers disease or other
XX CC nephropathies associated with Schönlein-Henoch purpura, celiac disease,
XX CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
XX CC to generate transgenic animals for use in development and screening of
XX CC therapeutically useful reagents and also for chromosome identification
XX CC and tissue typing.
XX SQ Sequence 134 AA;

Query Match 56.2%; Score 208.5; DB 21; Length 134;
Best Local Similarity 63.2%; Pred. No. 1e-17;
Matches 43; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

Qy 1 EKDIMLYNQPEPKVSKFLFYHQSQRNSTFESVAFPGWFIATVSSEGGCPILITQELGKAN 60
Db 66 eqkmdlyggpevpkpflyfraktrgtstlesvafpdwfiasskrdqpilttselgksy 124
Qy 61 TTDFGLTLM 68
Db 125 ntafelni 132

RESULT 12
AAY96935
ID AAY96935 standard; Protein; 134 AA.
XX AC AAY96935;
XX DT 31-OCT-2000 (first entry)
XX DE Human IL-1 receptor antagonist 2.
XX KW hIL-1ra2; human interleukin-1 receptor antagonist-2; IL-1lp; osteopathic;
XX KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
XX KW anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;
XX KW dermatological; immunomodulatory; gastrointestinal; gene therapy.
XX OS Homo sapiens.
XX PN WO200039297-A2.
XX PD 06-JUL-2000.
XX PF 22-DEC-1999; 99WO-US30720.
XX PR 23-DEC-1998; 98US-0113430.
XX PR 22-JAN-1999; 99US-0116843.
XX PR 13-APR-1999; 99US-0129122.
XX PA (GETH ) GENENTECH INC.
XX PI Goddard A, Pan J;
XX DR WPI; 2000-452395/39.
XX DR N-PSDB; AA51595.
XX PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
XX PT preventing and treating e.g. inflammation, asthma and psoriasis
XX PS Claim 22; Fig 5A-B; 143pp; English.
XX CC An isolated nucleic acid molecule encoding an interleukin-1-like
XX CC polypeptide (IL-1p) that retains one or more activities of the peptide
XX CC from which it is derived, such as the IL-18R binding activity of a human
XX CC interleukin-1 receptor antagonist-1 (hIL-1ra1) polypeptide, is new. The
XX CC nucleic acids may be used in molecular engineering applications, e.g.
XX CC hybridization assays and chromosome and gene mapping studies, for
XX CC recombinantly producing the IL-1p polypeptide or for producing gene
XX CC knock out animals to study the role of the protein in metabolism and
XX CC disease processes (conversely, gene therapy protocols may be used to
XX CC supplement a patients production of the polypeptide or to rectify
XX CC mutations that lead to the production of in active peptides). The
XX CC peptides produced may be used to screen for and produce modulators (e.g.
XX CC antibodies) of IL-1p protein expression and activity which may be use
XX CC to treat disorders associated with inappropriate IL-1p expression and
XX CC activity, such as inflammatory disorders, asthma, arthritis,
XX CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
XX CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
XX CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX SQ Sequence 134 AA;

Query Match 56.2%; Score 208.5; DB 21; Length 134;
Best Local Similarity 63.2%; Pred. No. 1e-17;
Matches 43; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

Qy 1 EKDIMLYNQPEPKVSKFLFYHQSQRNSTFESVAFPGWFIATVSSEGGCPILITQELGKAN 60
Db 66 eqkmdlyggpevpkpflyfraktrgtstlesvafpdwfiasskrdqpilttselgksy 124
Qy 61 TTDFGLTLM 68
Db 125 ntafelni 132

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RESULT	14
AAW63136	AAW63136
ID	AAW63136 standard; Protein; 169 AA.
XX	XX
AC	AC
AAW63136;	AAW63136;
XX	XX
14-OCT-1998	(first entry)
DT	DT
XX	XX
DE	DE
XX	XX
Interleukin-1 receptor antagonist beta (IL-1ra-beta).	
XX	XX
IL-1 beta; interleukin-1 receptor antagonist; IL-1ra-beta; IL-1 alpha;	
KW	KW
IL-1 beta; inflammatory response; treatment; inflammation; septicemia;	
KW	KW
cancer; anaemia; arthritis; inflammatory bowel disease;	
KW	KW
graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;	
KW	KW
acute respiratory disease syndrome; psoriasis; restenosis;	
KW	KW
traumatic brain injury; acquired immune deficiency syndrome;	
KW	KW
cachexia.	
XX	XX
Homo sapiens.	
OS	OS
EP855404-A1.	
PN	PN
29-JUL-1998.	
XX	XX
27-JAN-1998; 98EP-0300572.	
PF	PF
28-JAN-1997; 97US-0790032.	
XX	XX
(SMIK ) SMITHKLINE BEECHAM CORP.	
XX	XX
Young PR;	
PA	PA
WI; 1998-389778/34.	
DR	DR
N-PSDB; AAW42659.	
XX	XX
New nucleic acid encoding human interleukin-1 receptor antagonist	
PT	PT
beta polypeptides - and related expression systems, transformed	
PT	PT
cells, proteins, antibodies, agonists and antagonists, useful for	
PT	PT
treatment, prevention and diagnosis of inflammation, septicemia,	
PT	PT
cancer etc	
XX	XX
Claim 13; Fig 2; 20pp; English.	
PS	PS
XX	XX
The present sequence represents human Interleukin-1 receptor antagonist	
CC	CC
beta (IL-1ra-beta). IL-1 alpha and IL-1 beta play key roles in	
CC	CC
inflammatory responses, and are produced as zymogens which are cleaved	
CC	CC
upon secretion to yield mature carboxyl terminal 17 kb fragments.	
CC	CC
IL-1ra-beta polypeptides and polynucleotides are useful in treatment of	
CC	CC
chronic and acute inflammation, septicemia, cancer, anaemia, arthritis,	
CC	CC
inflammatory bowel disease, graft vs. host rejection, autoimmunity,	
CC	CC
stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),	
CC	CC
perforis, restenosis, traumatic brain injury, acquired immune	
CC	CC
deficiency syndrome (AIDS) and cachexia. These conditions (or	
CC	CC
susceptibility to them) may be diagnosed by detecting mutations in the	
CC	CC
IL-1ra-beta coding sequence analysing a sample for presence or amount	
CC	CC
of IL-1ra-beta.	
XX	XX
Sequence 169 AA;	
SQ	SQ
Query Match	56.2%; Score 208.5; DB 19; Length 169;
Best Local Similarity	63.2%; Pred. No. 1.4e-17;
Matches 43; Conservative	8; Mismatches 16; Indels 1; Gaps 1;
OY	1 EKIDIMLYNQPEVKFSLFVHSGSRNSTFESVAFPGWFIASVSGCGPLILITQELGRAN 60
Db	101 eqkimdlygpevpkpflyfyraktgrtstlesvafpdwfiia-sskrdpqiltselgkxy 159
OY	61 TTDFGLTM 68
Db	160 ntafeini 167

QY 1 EKDIMLYNQPEPVKSFLEFVHSGRNSTFESVAFPGWFIASVSGGCPILITLTOELGKAN 60  
 Db 101 eqkimdlyggpevpkpfllfyraktgrtstlesvafpdwfa-sskrdqpiiltseigksy 159  
 QY 61 TTDFGLTM 68  
 Db 160 ntafeini 167

RESULT 15  
 AAY24395  
 ID AAY24395 standard; Protein; 169 AA.  
 XX  
 AC AAY24395;  
 XX  
 DT 20-SRP-1999 (first entry)  
 XX  
 DE Human interleukin-1 receptor antagonist beta.  
 XX  
 KW Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;  
 KW chronic inflammation; acute inflammation; arthritis; autoimmunity;  
 KW inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;  
 KW cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;  
 KW traumatic brain injury; AIDS; cachexia; allergy; parasite infection;  
 KW allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;  
 KW allergic inflammatory disease; delayed hypersensitivity; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09936541-A1.  
 XX  
 PD 22-JUL-1999.  
 XX  
 PF 14-JAN-1999; 99WO-US00847.  
 XX  
 PR 29-APR-1998; 98US-0069619.  
 PR 14-JAN-1998; 98US-0007464.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Marshall L, Young PR;  
 XX  
 DR WPI: 1999-430615/36.  
 DR N-PSDB; AAX90135.  
 XX  
 PT New interleukin-1 receptor antagonist beta, useful for treating  
 PT inflammation and autoimmune diseases  
 XX  
 PS Claim 15; Fig 1; 34pp; English.  
 XX  
 CC The present sequence represents human interleukin-1 receptor antagonist  
 CC beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are  
 CC useful for diagnosing diseases (or susceptibility to diseases) related  
 CC to the expression or activity of IL-1RA beta, by determining mutations  
 CC in the IL-1RA beta nucleic acid sequences and/or analysing for the  
 CC presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides  
 CC are also useful for screening for compounds which affect activity of the  
 CC protein. These can be used in treatment to inhibit (antagonist) or  
 CC enhance (agonist) IL-1RA beta activity, in addition to direct  
 CC administration of IL-1RA beta polypeptides to treat conditions, or  
 CC direct administration of antisense sequences to prevent expression.  
 CC IL-1RA beta polypeptides (administered directly, in a vector i.e. gene  
 CC therapy, and as a vaccine) and antibodies induce an immune response to  
 CC immunise and prevent disease. Diseases diagnosed, prevented or treated  
 CC include chronic and acute inflammation, septicemia, arthritis,  
 CC inflammatory bowel disease, graft vs. host disease, autoimmunity,  
 CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),  
 CC psoriasis, restenosis, traumatic brain injury, AIDS, cachexia, allergy,  
 CC parasite infection, allergic rhinitis, allergic asthma, atopic  
 CC dermatitis, allergic inflammatory diseases and delayed hypersensitivity.  
 XX  
 SQ Sequence 169 AA;

Query Match 56.28; Score 208.5; DB 20; Length 169;  
 Best Local Similarity 63.2%; Pred. No. 1.4e-17;  
 Matches 43; Conservative 8; Mismatches 16; Indels 1; Gaps 1;  
 QY 1 EKDIMLYNQPEPVKSFLEFVHSGRNSTFESVAFPGWFIASVSGGCPILITLTOELGKAN 60  
 Db 101 eqkimdlyggpevpkpfllfyraktgrtstlesvafpdwfa-sskrdqpiiltseigksy 159  
 QY 61 TTDFGLTM 68  
 Db 160 ntafeini 167

Search completed: June 20, 2002, 15:03:07  
 Job time: 118 sec



Result No.	§			DB	ID	Description
	Query Match	Length	Score			
1	124	33.4	155	2	JC7104	interleukin-1 rece
2	107	28.8	177	2	A54377	interleukin-1 rece
3	107	28.8	178	2	C40956	interleukin-1 rece
4	105	28.3	178	2	A44610	interleukin-1 rece
5	101	27.2	177	2	A30368	interleukin-1 rece
6	101	27.2	180	2	A39386	interleukin-1 rece
7	96	25.9	267	1	JN0724	interleukin-1 beta
8	96	25.9	267	2	S38373	interleukin-1 beta
9	89	24.0	266	1	S23010	interleukin-1 beta
10	88	23.7	266	1	IC01B	interleukin-1 beta
11	85	22.9	269	1	ICHULB	interleukin-1 beta
12	81	21.8	214	2	JC5646	interleukin-1 beta
13	74	19.9	268	1	A30584	interleukin-1 beta
14	65.5	17.7	269	1	S5969	interleukin-1 beta
15	64.5	17.4	541	2	S56653	thioglycosidase (E
16	63	17.0	364	1	S77360	cblD protein - syn
17	62.5	16.8	268	1	IC01A	interleukin-1 alph
18	62.5	16.8	268	1	A61245	interleukin-1 alph
19	62.5	16.8	270	1	S10532	interleukin-1 alph
20	62.5	16.8	533	2	T19416	hypothetical prote
21	62	16.7	939	2	E82121	peptidase, insulin
22	61.5	16.6	325	2	E87125	ribonucleotide red
23	61	16.4	255	2	C95997	probable glucose-1
24	61	16.4	273	2	AB2150	hypothetical prote
25	61	16.4	522	2	C90073	hypothetical prote
26	61	16.4	1161	1	S31213	nitrogen precursor
27	60.5	16.3	1558	2	C89114	protein C37C3.6a [
28	60.5	16.3	2167	2	T34395	hypothetical prote
29	60	16.2	407	2	T22554	hypothetical prote

A;Title: Interleukin-1 recetor antagonist in inflammatory exudate cells of rabbits. P

<p>A:Reference number: I46729; MUID:93052512</p> <p>A:Accession: I46729</p> <p>A:Status: translated from GB/EMBL/DBDJ</p> <p>A:Molecule type: mRNA</p> <p>A:Residues: 1-177 &lt;GOT&gt;</p> <p>A:Cross-references: GB:D21832; NID:g425787; PIDN:BAA04860.1; PID:g452205</p> <p>C:Superfamily: Interleukin-1</p> <p>C:Keywords: cytokine receptor; extracellular protein; glycoprotein</p> <p>F;1-25/Domain: signal sequence #status predicted &lt;SIG&gt;</p> <p>F;109/Binding site: carbohydrate (Asn) (covalent) #status predicted</p> <p>Query Match 28.8%; Score 107; DB 2; Length 177;</p> <p>Best Local Similarity 41.0%; Pred. No. 1.6e-05;</p> <p>Matches 25; Conservative 6; Mismatches 24; Indels 6; Gaps 1;</p>	<p>Qy 3 DIMDLYNQPEPVKSFLEFVHSQSGRNSTFESVAFPGWFIASVSGGCPPLIILT 62</p> <p>Db 109 NITDGLNKEEDKRFITFIRNSGPTTFESASCPGWFLCTLEADQPVSLT-----NTP 162</p>	<p>Qy 63 D 63</p> <p>Db 163 D 163</p>	<p>RESULT 3</p> <p>C40356</p> <p>Interleukin-1 receptor antagonist precursor - rat</p> <p>C:Species: Rattus norvegicus (Norway rat)</p> <p>C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999</p> <p>C:Accession: C40956</p> <p>R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991</p> <p>A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family</p> <p>A:Reference number: A40956; MUID:91271363</p> <p>A:Accession: C40956</p> <p>A:Status: preliminary</p> <p>A:Molecule type: DNA</p> <p>A:Residues: 1-178 &lt;ETS&gt;</p> <p>A:Cross-references: GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g204929</p> <p>C:Superfamily: interleukin-1</p> <p>C:Keywords: cytokine receptor</p> <p>Query Match 28.8%; Score 107; DB 2; Length 178;</p> <p>Best Local Similarity 41.5%; Pred. No. 1.6e-05;</p> <p>Matches 22; Conservative 9; Mismatches 22; Indels 0; Gaps 0;</p>	<p>Qy 1 EKDIMLYNQPEPVKSFLEFVHSQSGRNSTFESVAFPGWFIASVSGGCPPLIILT 53</p> <p>Db 108 EVNITDLNKEEDKRFITFIRSETGPTTFESACPGWFLCTTLEADHPVSLT 160</p>	<p>RESULT 4</p> <p>A44610</p> <p>Interleukin-1 receptor antagonist precursor - mouse</p> <p>N:Alternate names: IL-1ra</p> <p>C:Species: Mus musculus (house mouse)</p> <p>C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999</p> <p>C:Accession: A44610; A40956; A49031; I56106; I52970</p> <p>R:Matsumine, H.; Rousssel, M.F.; Matsushima, K.; Sherr, C.J. Blood 78, 616-623, 1991</p> <p>A:Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrophage</p> <p>A:Reference number: A44610; MUID:91316273</p> <p>A:Accession: A44610</p> <p>A:Molecule type: mRNA</p> <p>A:Residues: 1-178 &lt;MAT&gt;</p> <p>A:Cross-references: GB:M64404; NID:g198296; PIDN:AAA39277.1; PID:g198297</p> <p>R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991</p> <p>A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family</p> <p>A:Reference number: A40956; MUID:91271363</p> <p>A:Accession: B40956</p>	<p>A:Molecule type: DNA</p> <p>A:Residues: 7-178 &lt;ETS&gt;</p> <p>A:Cross-references: GB:M63100; NID:g198389; PIDN:AAA39310.1; PID:g198390</p> <p>R:Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J. Eur. J. Immunol. 21, 2775-2780, 1991</p> <p>A:Title: Cloning, heterologous expression and characterization of murine interleukin 1</p> <p>A:Reference number: A49031; MUID:92037824</p> <p>A:Accession: A49031</p> <p>A:Molecule type: mRNA</p> <p>A:Residues: 23-178 &lt;SHU&gt;</p> <p>A:Cross-references: GB:S64082; NID:g238584; PIDN:AAB20265.1; PID:g238585</p> <p>A:Experimental source: peritoneal macrophages, ICR strain</p> <p>A:Note: sequence extracted from NCBI backbone (NCBIN:64082, NCBI:P:64085)</p> <p>R:Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S. J. Immunol. 146, 4228-4233, 1991</p> <p>A:Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene map</p> <p>A:Reference number: I56106; MUID:91250712</p> <p>A:Accession: I56106</p> <p>A:Status: preliminary; translated from GB/EMBL/DBDJ</p> <p>A:Molecule type: mRNA</p> <p>A:Residues: 1-178 &lt;RES&gt;</p> <p>A:Cross-references: GB:M74294; NID:g198387; PIDN:AAA39309.1; PID:g198388</p> <p>R:Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S. Cytokine 6, 1-9, 1994</p> <p>A:Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulation</p> <p>A:Reference number: I52970; MUID:94271931</p> <p>A:Accession: I52970</p> <p>A:Status: preliminary; translated from GB/EMBL/DBDJ</p> <p>A:Molecule type: DNA</p> <p>A:Residues: 1-178 &lt;RES&gt;</p> <p>A:Cross-references: GB:L32839; NID:g487864; PIDN:AAA20576.1; PID:g528978</p> <p>C:Genetics:</p> <p>A:Gene: IL-1rn</p> <p>A:Introns: 40/2; 70/1; 107/3</p> <p>C:Superfamily: interleukin-1</p> <p>C:Keywords: cytokine receptor</p> <p>F;1-26/Domain: signal sequence #status predicted &lt;SIG&gt;</p> <p>F;27-178/Product: interleukin-1 receptor antagonist #status predicted &lt;MA2&gt;</p> <p>Query Match 28.3%; Score 105; DB 2; Length 178;</p> <p>Best Local Similarity 41.5%; Pred. No. 2.9e-05;</p> <p>Matches 22; Conservative 7; Mismatches 24; Indels 0; Gaps 0;</p>	<p>Qy 1 EKDIMLYNQPEPVKSFLEFVHSQSGRNSTFESVAFPGWFIASVSGGCPPLIILT 53</p> <p>Db 108 EVNITDLNKEEDKRFITFIRSEKPTTFESACPGWFLCTTLEADRPVSLT 160</p>	<p>RESULT 5</p> <p>A30368</p> <p>Interleukin-1 receptor antagonist secreted form precursor - human</p> <p>C:Species: Homo sapiens (man)</p> <p>C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000</p> <p>C:Accession: A40956; I37894; A30368; S08160; S08159; A37822</p> <p>R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991</p> <p>A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family</p> <p>A:Reference number: A40956; MUID:91271363</p> <p>A:Accession: A40956</p> <p>A:Molecule type: DNA</p> <p>A:Residues: 1-177 &lt;EIS&gt;</p> <p>A:Cross-references: GB:M63099; NID:g186385; PIDN:AAB41943.1; PID:g186386</p> <p>R:Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari, Cytokine 4, 83-89, 1992</p> <p>A:Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist</p> <p>A:Reference number: I37894; MUID:92338323</p> <p>A:Accession: I37894</p> <p>A:Status: translated from GB/EMBL/DBDJ</p> <p>A:Molecule type: DNA</p> <p>A:Residues: 1-177 &lt;LEN&gt;</p> <p>A:Cross-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799</p> <p>R:Carter, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom</p>
--	---	---------------------------------------	---	--	--	--	---	---

Query Match	25.9%	Score 96;	DB 1;	Length 267;
Best Local Similarity	30.6%;	Pred. No.	0.00057;	
Matches	19;	Conservative	13;	Mismatches 30; Indels 0; Gaps 0;
Qy	8	YNQPEPVKSFLEFYHSQSGRNSTFESVAPPGWFIASVSEGGCPLILTOELGKANTTDGLT	67	
	I : I : I : I :	:     :   :	I : I : I :	
Db	204	YPKRDMKRFFVFYKTEIKNRVEFSALYPNNYISTSAEQKVPFLGNKSRQDITDTME	263	
Qy	68	ML	69	
	:	I		
Db	264	VL	265	

```
RESULT 8
S38373
interleukin-1 beta precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C:Accession: S38373
R:Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Opde
Eur. J. Biochem. 217, 45-52, 1993
A:Title: Gene sequence, cDNA construction, expression in Escherichia coli and geneticall
A:Reference number: S38373; MUID:94039070
A:Accession: S38373
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-267 <VAN>
A:Cross-references: EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g407900
C:Genetics:
A:Introns: 16/2; 33/3; 99/1; 154/1; 197/3
C:Superfamily: Interleukin-1

Query Match 25.9%; Score 96; DB 2; Length 267;
Best Local Similarity 30.6%; Pred. No. 0.00057;
Matches 19; Conservative 13; Mismatches 30; Indels 0; Gaps 0;

QY 8 YNQPVPKSLFYHSQSGRNSTFESVAFPGWFIAVSSEGCGPLILTOELGKANTDFTGLT 67
DB 204 YPKRDMKEKRFVYKTEIKNRVEFESALYPNWIYSTQAEQKPVFLGNSKGRQDITDFTWE 263
QY 68 ML 69
DB 264 VL 265

RESULT 9
S23010
interleukin-1 beta precursor - sheep
N:Alternate names: hematopoietin-1; IL-1 beta
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999
C:Accession: S23010; S43047; S13092; B61246
R:Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A:Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
A:Reference number: S23010; MUID:92119335
A:Accession: S23010
A:Molecule type: mRNA
A:Residues: 1-266 <SEO>
A:Cross-references: EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809
A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an addi
submitted to the EMBL Data Library, May 1992
R:Sargan, D.R.
A:Reference number: S43047
A:Accession: S43047
A:Molecule type: mRNA
A:Residues: 1-13, 'C', 15-54, 'K', 56-63, 'A', 65-144, 'L', 146-266 <SAR>
A:Cross-references: EMBL:X54796; NID:g1273; PIDN:CAA38566.1; PID:g1274
R:Fiskerstrand, C.; Sargan, D.
Nucleic Acids Res. 18, 7165, 1990
A:Title: Nucleotide sequence of ovine interleukin-1 beta.
A:Reference number: S13092; MUID:91088326
A:Accession: S13092
A:Molecule type: mRNA
A:Residues: 1-13, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'L', 146-266 <FIS>
A:Cross-references: EMBL:X54796
A:Note: the authors translated the codon AGT for residue 62 as Arg
R:Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
Immunology 74, 453-460, 1991
A:Title: Molecular cloning and characterization of ovine IL-lalpha and IL-lbeta.
A:Reference number: A61246; MUID:92120716
A:Accession: B61246
A:Molecule type: mRNA
A:Residues: 1-144, 'L', 146-266 <AND>
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
```

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ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive.
C:Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin
C:Genetics:
A:Gene: IL-1-beta
C:Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F:114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match 24.0%; Score 89; DB 1; Length 266;
Best Local Similarity 31.7%; Pred. No. 0.004;
Matches 20; Conservative 12; Mismatches 31; Indels 0; Gaps 0;

QY 7 LYNQPEPKSLFYHSQSGRNSTFESVAFPGWFIAVSSEGCGPLILTOELGKANTDFTGL 66
DB 202 VYPKRNMEKRFVYKTEIKNTVEFESVLPNWIYSTQIEEKPVFLGFRGGQDITDFRM 261
QY 67 TML 69
DB 262 ETL 264

RESULT 10
ICBO1B
interleukin-1 beta precursor - bovine
N:Alternate names: hematopoietin-1; IL-1 beta
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C:Accession: J10010; S01380
R:Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, .
Mol. Immunol. 25, 429-437, 1988
A:Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleuk
A:Reference number: A94695; MUID:88318652
A:Accession: J10010
A:Molecule type: mRNA
A:Residues: 1-266 <MAL>
A:Cross-references: GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
R:Leong, S.R.; Flaggs, G.M.; Lawman, M.; Gray, P.W.
Nucleic Acids Res. 16, 9054, 1988
A:Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.
A:Reference number: S01380; MUID:89016591
A:Accession: S01380
A:Molecule type: mRNA
A:Residues: 1-251, 'A', 253-266 <LEO>
A:Cross-references: EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:g449
C:Comment: This protein is a cytokine that mediates a variety of immunoregulatory and
C:Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive.
C:Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin
C:Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F:114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match 23.7%; Score 88; DB 1; Length 266;
Best Local Similarity 31.7%; Pred. No. 0.0053;
Matches 20; Conservative 11; Mismatches 32; Indels 0; Gaps 0;

QY 7 LYNQPEPKSLFYHSQSGRNSTFESVAFPGWFIAVSSEGCGPLILTOELGKANTDFTGL 66
DB 202 VYPKRNMEKRFVYKTEIKNTVEFESVLPNWIYSTQIEERPVFLGFRGGQDITDFRM 261
QY 67 TML 69
DB 262 ETL 264

RESULT 11
ICBU1B
interleukin-1 beta precursor [validated] - human
N:Alternate names: hematopoietin-1; IL-1 beta
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1986 #sequence_revision 15-May-1998 #text_change 15-Sep-2000
```

C:Accession: A25542; A29019; A94023; A93361; I51852; I65200; I38132; B27616; A01848; S19  
 R:Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.  
 Nucleic Acids Res. 14, 7897-7914, 1986  
 A:Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev  
 A:Reference number: A25542; MUID:87040762  
 A:Accession: A25542  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-5, 'K', 7-269 <CIA>  
 A:Cross-references: GB:X04500  
 A:Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu  
 R:Bensi, G.; Raugel, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Melli, M.  
 Gene 52, 95-101, 1987  
 A:Title: Human interleukin-1 beta gene.  
 A:Reference number: A29019; MUID:87248099  
 A:Accession: A29019  
 A:Molecule type: DNA  
 A:Residues: 1-269 <BEN>  
 A:Cross-references: GB:M15840; NID:g186281; PIDN:AAA74137.1; PID:g386816  
 R:Auron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinarello, C.A.;  
 Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984  
 A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.  
 A:Reference number: A94023; MUID:85088517  
 A:Accession: A94023  
 A:Molecule type: mRNA  
 A:Residues: 1-5, 'K', 7-269 <AUR>  
 A:Cross-references: GB:X02770; NID:g186268; PIDN:AAA36106.1; PID:g307043  
 R:March, C.J.; Moseley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S.  
 Nature 315, 641-647, 1985  
 A:Title: Cloning, sequence and expression of two distinct human interleukin-1 complement  
 A:Reference number: A93361; MUID:85240547  
 A:Accession: A93361  
 A:Molecule type: mRNA  
 A:Residues: 1-269 <MAR>  
 A:Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1; PID:g33790  
 A:Note: parts of this sequence, including the amino end of the mature form, were confirm  
 R:Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au  
 Adv. Gene Technol. 22, 339-340, 1985  
 A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.  
 A:Reference number: I51852  
 A:Accession: I51852  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'O', 112-176, 'A', 178-213, 'P', 215-269 <WEB>  
 A:Cross-references: GB:M54933; NID:g186287; PIDN:AAA59136.1; PID:g186288  
 R:Nishida, T.; Nishino, M.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; Hira  
 Biochem. Biophys. Res. Commun. 143, 345-352, 1987  
 A:Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.  
 A:Reference number: I52217; MUID:87156769  
 A:Accession: I65200  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-269 <NIS>  
 A:Cross-references: GB:M15330; NID:g186283; PIDN:AAA59135.1; PID:g307045  
 R:Kotenko, S.V.; Bulenkov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov,  
 Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989  
 A:Title: Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin  
 A:Reference number: I38131; MUID:90249285  
 A:Accession: I38132  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-269 <KOT>  
 A:Cross-references: EMBL:X56087; NID:g335662; PIDN:CAA39567.1; PID:g335663  
 R:Zebo, K.M.; Wypych, J.; Yushenko, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K.  
 Blood 71, 962-968, 1988  
 A:Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic  
 A:Reference number: A90732; MUID:88184226  
 A:Accession: B27616  
 A:Molecule type: protein  
 A:Residues: 117-123, 'X', 125-126, 'X', 128 <ZSE>  
 R:Stevenson, F.T.; Bursten, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993  
 A:Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysines

A:Reference number: A48293; MUID:93348250  
 A:Contents: annotation; myristylation of lysines  
 R:Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.  
 Biochim. Biophys. Acta 1118, 25-35, 1991  
 A:Title: The role of arginine residues in interleukin 1 receptor binding.  
 A:Reference number: S19608; MUID:92110334  
 A:Contents: annotation; type 1 IL-1 receptor interaction site  
 A:Note: modification of Arg-120 by phenylglyoxal blocks receptor binding  
 R:Clare, G.M.; Gronenborn, A.M.  
 submitted to the Brookhaven Protein Data Bank, January 1991  
 A:Reference number: A50049; PDB:611B  
 A:Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269  
 R:Clare, G.M.; Wingfield, P.T.; Gronenborn, A.M.  
 Biochemistry 30, 2315-2323, 1991  
 A:Title: High-resolution three-dimensional structure of interleukin 1beta in solution  
 A:Reference number: A44675; MUID:91159409  
 A:Contents: annotation; (1)H-NMR structural determination  
 R:Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.  
 J. Biol. Chem. 266, 7081-7086, 1991  
 A:Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a  
 A:Reference number: A39774; MUID:91201363  
 A:Contents: annotation  
 R:Finzel, B.C.; Watenpau, K.D.; Einspahr, H.M.  
 submitted to the Brookhaven Protein Data Bank, December 1989  
 A:Reference number: A50016; PDB:111B  
 A:Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269  
 R:Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpau, K.D.; Einspa  
 J. Mol. Biol. 209, 779-791, 1989  
 A:Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom res  
 A:Reference number: A44666; MUID:90064532  
 A:Contents: annotation; X-ray crystallography, 2.0 angstroms  
 C:Comment: This protein lacks a conventional signal sequence for protein export. Clea  
 ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.  
 C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin  
 C:Genetics:  
 A:Gene: GDB:IL1B  
 A:Cross-references: GDB:I20094; OMIM:147720  
 A:Map position: 2q13-2q21  
 A:Introns: 16/2; 33/3; 101/1; 156/1; 199/3  
 C:Superfamily: Interleukin-1  
 C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macroph  
 F:117-269/Product: interleukin-1 beta #status experimental <IL1>  
 F:76/Binding site: myristate (Lys) (covalent) (partial) #status experimental  
 F:123/Binding site: carbohydrate (Asn) (covalent) #status absent  
 Query Match 22.9%; Score 85; DB 1; Length 269;  
 Best Local Similarity 33.3%; Pred. No. 0.012;  
 Matches 21; Conservative 8; Mismatches 32; Indels 2; Gaps 1;  
 QY 8 YNQPEPVKSFYHSGSGRNSTFESVAFPGWFIASVSGGCPILITQELGRANTTDFGLT 67  
 DB 206 YPKKMKERFVNKINNKLEFESAQFPNWIISTQAEINMPVFLGGTKGGQDITDF--T 263  
 QY 68 MLF 70  
 DB 264 MQF 266  
 RESULT 12  
 JC5646  
 Interleukin-1 beta - horse  
 C:Species: Equus caballus (domestic horse)  
 C:Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 20-Jun-2000  
 C:Accession: JC5646  
 R:Kato, H.; Yoon, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa  
 Gene 177, 11-16, 1996  
 A:Title: Identification of an alternatively spliced transcript of equine interleukin-  
 A:Reference number: JC5646; MUID:97080493  
 A:Accession: JC5646  
 A:Molecule type: mRNA  
 A:Residues: 1-214 <KAT>  
 A:Cross-references: DDBJ:D42165; NID:g2463549; PIDN:BAA22528.1; PID:g2463550

;Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for mu  
 ;Reference number: I55969; MUID:87058957  
 ;Accession: I55969

Job time: 161 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:03:55 ; Search time 19.43 Seconds  
(without alignments)  
139.494 Million cell updates/sec

Title: US-09-763-498-6

Sequence: 1 ERKDMLYNQPEPVKSFLFY.....ILTQELGRANTTDFGLTMLF 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	28.8	177	1 IL1X_HORSE	Q18999 equus caball
2	107	28.8	177	1 IL1X_RABIT	P26890 eryctolagus
3	107	28.8	178	1 IL1X_RAT	P25086 rattus norv
4	105	28.3	178	1 IL1X_MOUSE	P25085 mus musculu
5	102	27.5	177	1 IL1X_PIG	Q29056 sus scrofa
6	101	27.2	177	1 IL1X_HUMAN	P18510 homo sapien
7	96	25.9	267	1 IL1B_PIG	P26889 sus scrofa
8	95	25.6	174	1 IL1X_BOVIN	O77482 bos taurus
9	89	24.0	266	1 IL1B_SHEEP	P21621 ovis aries
10	88	23.7	266	1 IL1B_CAPI	P79182 capra hircu
11	87	23.5	266	1 IL1B_CEREL	P51745 cervus elap
12	86	23.2	267	1 IL1B_FELCA	P41687 felis silve
13	85	22.9	268	1 IL1B_MACFA	P79182 macaca fasc
14	85	22.9	269	1 IL1B_HUMAN	P01584 homo sapien
15	85	22.9	269	1 IL1B_MACMU	P48090 macaca mula
16	85	22.9	269	1 IL1B_MACNE	P51493 macaca neme
17	82	22.1	266	1 IL1B_BOVIN	P09428 bos taurus
18	81	21.8	268	1 IL1B_HORSE	Q28386 equus cabal
19	77.5	20.9	269	1 IL1B_TRIVU	Q9xs77 trichosurus
20	77	20.8	269	1 IL1B_CERTO	P46648 cercocebus
21	74	19.9	268	1 IL1B_RABIT	P14628 eryctolagus
22	71.5	19.3	266	1 IL1B_CAVPO	Q9wvdl cavia porce
23	66.5	17.9	268	1 IL1B_RAT	Q63264 rattus norv
24	65.5	17.7	269	1 IL1B_MOUSE	P10749 mus musculu
25	65.5	17.7	270	1 IL1A_FELCA	O46613 felis silve
26	64.5	17.4	541	1 MYRO_ARATH	P37702 arabidopsis
27	62.5	16.8	268	1 IL1A_BOVIN	P08831 bos taurus
28	62.5	16.8	268	1 IL1A_CAPI	P79161 capra hircu
29	62.5	16.8	268	1 IL1A_SHEEP	Q28579 ovis aries
30	62.5	16.8	270	1 IL1A_HORSE	Q28385 equus cabal
31	62.5	16.8	270	1 IL1A_PIG	P18430 sus scrofa
32	61.5	16.6	325	1 RIR2_MYCLE	Q9cbx2 mycobacteri
33	60.5	16.3	265	1 IL1A_CANFA	O46612 canis famil

34	60.5	16.3	872	1 MGR2_HUMAN	Q14416 homo sapien
35	60	16.2	444	1 KRAC_DICDI	P54644 dictyosteli
36	59.5	16.0	634	1 YGJI_CAEEL	Q9xub9 caenorhabdi
37	58.5	15.8	271	1 IL1A_HUMAN	P01583 homo sapien
38	58	15.6	267	1 IL1A_RABIT	P04822 oryctolagus
39	58	15.6	453	1 PSNH_ARATH	O64668 arabidopsis
40	57.5	15.5	271	1 IL1A_MACFA	P79340 macaca fasc
41	57.5	15.5	413	1 ARCA_CLOPE	Q46254 clostridium
42	57	15.4	271	1 IL1A_MACMU	P48089 macaca mula
43	57	15.4	605	1 VEI_HPVO9	Q05111 human papil
44	56	15.1	419	1 VS48_TBRVC	P22048 tomato blac
45	56	15.1	459	1 CBIA_SALTY	P29946 salmonella

## ALIGNMENTS

RESULT	1				
IL1X_HORSE					
ID	IL1X_HORSE	STANDARD;	PRT;	177 AA.	
AC	O18999; O77745;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)				
DE	(IRAP).				
GN	IL1RN OR IL1RA.				
OS	Equus caballus (Horse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.				
OX	NCBI_TaxID=9796;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97366446; PubMed=9223227;				
RA	Kato H., Ohashi T., Matsushiro H., Watari T., Goitsuka R.,				
RA	Tsujimoto H., Hasegawa A.;				
RT	"Molecular cloning and functional expression of equine interleukin-1				
RT	receptor antagonist.";				
RL	Vet. Immunol. Immunopathol. 56:221-231(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98285942; PubMed=9622739;				
RA	Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;				
RT	"Cloning of equine interleukin-1 receptor antagonist and				
RT	determination of its full-length cDNA sequence.";				
RL	Am. J. Vet. Res. 59:712-716(1998).				
CC	-I- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS				
CC	RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.				
CC	-I- SIMILARITY: BELONGS TO THE IL-1 FAMILY.				
CC	-----				
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL; D83714; BAA22529.1; -				
DR	EMBL; U92482; AAC39257.1; -				
DR	HSSP; P18510; IL1R				
DR	InterPro: IPR000975; Interleukin_1.				
DR	Pfam; PF00340; IL1; 1.				
DR	PRINTS; PR00264; INTERLEUKIN1.				
DR	ProDom; PD002536; Interleukin_1; 1.				
DR	SMART; SM00125; IL1; 1.				
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.				
DR	Glycoprotein; Signal.				
FT	SIGNAL	1	25		BY SIMILARITY.
FT	CHAIN	26	177		INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT					PROTEIN.
FT					BY SIMILARITY.
FT	DISULFID	91	141		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	109	109		

FT	SIGNAL		1	25	BY SIMILARITY.
FT	CHAIN		26	177	INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN.
FT					
FT	DISULFID		91	141	BY SIMILARITY.
FT	CARBOHYD		109	109	N-LINKED (GLCNAC...)(POTENTIAL).
FT	SEQUENCE		177 AA;	20214 MW; F5BC08F097FFFAFCRC64;	
SQL					
	Query Match				
	Best Local Similarity				28.8%; Score 107; DB 1; Length 177;
	Matches		25; Conservative	6; Mismatches	24; Indels
					Gaps
					1;
QY	3 DIMDLYNQPPEVFSFLPYHSOSGRNSTFESVAFPGWFIANSSEGGCLPIITQLGKANTT	62			
	:      :       :       :       :       :       :				
Db	109 NITDGLGNKEQDKRFTIRNSGPTTTTFESASCSPGWFLCTALEADQPVSLT-----NTP	162			
QY	63 D 63				
Db	163 D 163				
RESULT	3				
ILIX_RAT					
ID	ILIX_RAT	STANDARD;	PRT:	178 AA.	
AC	P25086;				
DT	01-MAY-1992 (Rel. 22, Created)				
DT	01-MAY-1992 (Rel. 22, Last sequence update)				
DT	01-NOV-1995 (Rel. 32, Last annotation update)				
DE	Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)				
DE	(IRAP).				
GS	IL1RN OR IL-1RA.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_TaxID=10116;				
[1]					
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91271363; PubMed=1828896;				
RA	Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,				
RA	Brandhuber B.J., Thompson R.C.;				
RT	"Interleukin 1 receptor antagonist is a member of the interleukin 1				
RT	gene family: evolution of a cytokine control mechanism.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).				
-I-	FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS				
CC	RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.				
-I-	SIMILARITY: BELONGS TO THE IL-1 FAMILY.				
CC					
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to licensedisb@sib.ch).				
CC					
DR	EMBL; MG3101; AAA41434.1; ..				
DR	PIR; C40956; C40956.				
DR	HSSP; PI8510; IL1R.				
DR	InterPro; IPR000975; Interleukin_1.				
DR	Pfam; PF00340; IL1; 1.				
DR	PRINTS; PR00264; INTERLEUKIN1.				
DR	ProDom; PD002536; Interleukin_1; 1.				
DR	SMART; SM00125; IL1; 1.				
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.				
KW	Glycoprotein; Signal.				
FT	SIGNAL		1	26	BY SIMILARITY.
FT	CHAIN		27	178	INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN.
FT					
FT	DISULFID		92	142	BY SIMILARITY.
FT	CARBOHYD		110	110	N-LINKED (GLCNAC...)(POTENTIAL).
SQL	SEQUENCE		178 AA;	20282 MW; F3A5754FB6C51B03 CRC64;	

Query Match 28.8%; Score 107; DB 1; Length 178;  
Best Local Similarity 41.5%; Pred. No. 2.9e-06;  
Matches 22; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 1 EKIDIMLYNQPEPVKSFYFHQSQRNSTFESVAFPGWFIASVSGGCPILIT 53  
| : | | | | : | | : | | | | | | | : | | | |  
Db 108 EVNITDLNKNKEEDKRFIFIRSTGPTTSFESLACPGWFLCTTLEADRPVSLT 160

RESULT 4  
IL1X\_MOUSE  
ID IL1X\_MOUSE STANDARD; PRT; 178 AA.  
AC P25085; 070207;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-MAY-2002 (Rel. 41, Last annotation update)  
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)  
DE (IRAP).  
OS IL1RN OR IL-1RA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RP MEDLINE=91250712; PubMed=1828262;  
RA Zahedi K., Seldin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;  
RT "Mouse IL-1 receptor antagonist protein. Molecular characterization,  
RT gene mapping, and expression of mRNA in vitro and in vivo.";  
RL J. Immunol. 146:4228-4233(1991).  
[2]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RP MEDLINE=91316273; PubMed=1830498;  
RA Matsushima H., Rousset M.F., Matsushima K., Hishinuma A., Sherr C.J.;  
RT "Cloning and expression of murine interleukin-1 receptor antagonist  
RT in macrophages stimulated by colony-stimulating factor 1.";  
RL Blood 78:616-623(1991).  
[3]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RP STRAIN=SWISS;  
RC MEDLINE=94271931; PubMed=8003626;  
RA Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;  
RT "The mouse interleukin 1 receptor antagonist protein: gene structure  
RT and regulation in vitro.";  
RL Cytokine 6:1-9(1994).  
[4]  
RN SEQUENCE FROM N.A. (ISOFORM 2).  
RC STRAIN=FVBXDBA/1 LAGJ;  
RX MEDLINE=98209757; PubMed=9550387;  
RA Gabay C., Porter B., Fantuzzi G., Arend W.P.;  
RT "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning  
RT and protein expression of intracellular isoform and tissue  
RT distribution of secreted and intracellular IL-1 receptor antagonist in  
RT vivo.";  
RL J. Immunol. 159:5905-5913(1997).  
[5]  
RN SEQUENCE OF 7-178 FROM N.A.  
RX MEDLINE=91271363; PubMed=1828896;  
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,  
RA Brandhuber B.J., Thompson R.C.;  
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1  
RT gene family: evolution of a cytokine control mechanism.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).  
[6]  
RN SEQUENCE OF 23-178 FROM N.A.  
RX MEDLINE=92037824; PubMed=1834470;  
RA Shuck M.E., Bessalu T.E., Tracey D.E., Bienkowski M.J.;  
RT "Cloning, heterologous expression and characterization of murine  
RT interleukin 1 receptor antagonist protein.";  
RL Eur. J. Immunol. 21:2775-2780(1991).  
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS  
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.  
CC -!- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR

(ISOFORM 2).  
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are  
CC produced by alternative splicing.  
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
CC -----  
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CC -----  
CC EMBL; M74294; AAA39309.1; -  
CC EMBL; M64404; AAA39277.1; -  
CC EMBL; L32838; AAA20576.1; -  
CC EMBL; AF001795; AAC15251.1; -  
CC EMBL; M57525; AAA39278.1; -  
CC EMBL; M63100; AAA39310.1; -  
CC EMBL; S64082; AAB20265.1; -  
CC PIR; B40956; B40956.  
CC PIR; A44610; A44610.  
CC HSSP; P18510; IIRA.  
CC MGD; MGI:96547; Il1rn.  
CC InterPro: IPR000975; Interleukin\_1.  
CC Pfam; PF00340; IL1; 1.  
CC PRINTS; PR00264; INTERLEUKIN1.  
CC PRODOM; PD002536; Interleukin\_1; 1.  
CC SMART; SM00125; IL1; 1.  
CC PROSITE; PS00253; INTERLEUKIN\_1; 1.  
KW Glycoprotein; Signal; Alternative splicing.  
FT SIGNAL 1 26 BY SIMILARITY.  
FT CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST  
FT PROTEIN.  
FT DISULFID 92 142 BY SIMILARITY.  
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 1 21 MEICWGPYSHLSLLILLFHF -> MA (IN ISOFORM  
FT 2).  
SQ SEQUENCE 178 AA; 20274 MW; 84AA002A3119C024 CRC64;

Query Match 28.3%; Score 105; DB 1; Length 178;  
Best Local Similarity 41.5%; Pred. No. 5.2e-06;  
Matches 22; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

QY 1 EKIDIMLYNQPEPVKSFYFHQSQRNSTFESVAFPGWFIASVSGGCPILIT 53  
| : | | | | : | | : | | | | | | | : | | | |  
Db 108 EVNITDLNKNKEEDKRFIFIRSTGPTTSFESAACPGWFLCTTLEADRPVSLT 160

RESULT 5  
IL1X\_PIG  
ID IL1X\_PIG STANDARD; PRT; 177 AA.  
AC Q29056;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)  
DE (IRAP).  
GN IL1RN OR IRAP1.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=CROSSBREED; TISSUE=Lung;  
RA Yin J., Murtaugh M.P.;  
RT "Characterization of IRAP in morphine treated pig.";  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS  
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.  
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.

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CC -----
DR EMBL: L38849; AAA99424.1; -.
DR HSSP: P18510; ILIRA.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR PRINTS: PR00264; INTERLEUKIN1.
DR PRODOM: PD002536; Interleukin_1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 177
FT -----
FT BY SIMILARITY.
FT INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT -----
FT DISULFID 91 141
FT CARBOHYD 109 109
FT SEQUENCE 177 AA; 20093 MW; 2114DC6119A9DSF9 CRC64;
SQ SEQUENCE 177 AA; 20093 MW; 2114DC6119A9DSF9 CRC64;

Query Match 27.5%; Score 102; DB 1; Length 177;
Best Local Similarity 43.1%; Pred. No. 1.2e+05;
Matches 22; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

Qy 3 DIMLYNQPEPVKFLYHSGSGRNSTFESVAFPGWFIYVSSEGGCPILIT 53
:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 103 NITDLRKNSEQDKRFTIRSDSGTTSFESAACPGWFLCTALEADQPVGLT 159

RESULT 6
IL1X_HUMAN
ID IL1X_HUMAN STANDARD; PRT; 177 AA.
AC P18510; Q14628; Q9UPC0;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (ICIL-
DE IRA) (IRAP) (IL-1RN).
GN IL1RN OR ILIRA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90220867; PubMed=2139180;
RA Carter D.B., Deibel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
RA Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N.,
RA Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Sieu L.C.,
RA Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinrichson R.L.,
RA Truesdell S.E., Shelly J.A., Eessalu T.E., Taylor B.M., Tracey D.E.;
RA "Purification, cloning, expression and biological characterization of
RA an interleukin-1 receptor antagonist protein.";
RL Nature 344:633-638(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90136921; PubMed=2137201;
RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
RA Hannum C.H., Thompson R.C.;
RA "Primary structure and functional expression from complementary DNA
RT of a human interleukin-1 receptor antagonist.";
RL Nature 343:341-346(1990).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91271363; PubMed=1828896;
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandhuber B.J., Thompson R.C.;

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RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT gene family: evolution of a cytokine control mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=9233823; PubMed=1385987;
RA Lennard A., Gorman P., Carrier M., Griffiths S., Scotney H.,
RA Sheer D., Solari R.;
RT "Cloning and chromosome mapping of the human interleukin-1 receptor
RT antagonist gene.";
RL Cytokine 4:83-89(1992).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RX MEDLINE=971146044; PubMed=8992991;
RA Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
RA Arend W.P., Smith M.F. Jr.;
RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
RT and inducible regulatory regions.";
RL J. Immunol. 158:748-755(1997).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=91219436; PubMed=1827201;
RA Haskill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
RT "cDNA cloning of an intracellular form of the human interleukin 1
RT receptor antagonist associated with epithelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=95355865; PubMed=7629520;
RA Muzio M., Polentarutti N., Sironi M., Poli G., De Gioia L.,
RA Introna M., Mantovani A., Colotta F.;
RT "Cloning and characterization of a new isoform of the interleukin 1
RT receptor antagonist.";
RL J. Exp. Med. 182:623-628(1995).
RN [8]
RP SEQUENCE OF 26-45.
RX MEDLINE=90136920; PubMed=2137200;
RA Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J.,
RA Heimdal P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
RT "Interleukin-1 receptor antagonist activity of a human interleukin-1
RT inhibitor.";
RL Nature 343:336-340(1990).
RN [9]
RP SEQUENCE OF 26-52.
RX MEDLINE=90354444; PubMed=2143761;
RA Bienkowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
RA Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
RA Heinrichson R.L., Chosay J.G., Tracey D.E.;
RT "Purification and characterization of interleukin 1 receptor level
RT antagonist proteins from THP-1 cells.";
RL J. Biol. Chem. 265:14505-14511(1990).
RN [10]
RP SEQUENCE OF 35-177 FROM N.A. (ISOFORM 4).
RX MEDLINE=98183404; PubMed=9514884;
RA Weissbach L., Tran K., Colquhoun S.A., Champliand M.F., Towle C.A.;
RT "Detection of an interleukin-1 intracellular receptor antagonist mRNA
RT variant.";
RL Biochem. Biophys. Res. Commun. 244:91-95(1998).
RN [11]
RP STRUCTURE BY NMR.
RX MEDLINE=92297633; PubMed=1534997;
RA Stockman B.J., Scahill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
RA Brunner D.P., Yem A.W., Deibel M.R. Jr.;
RT "Secondary structure and topology of interleukin-1 receptor
RT antagonist protein determined by heteronuclear three-dimensional NMR
RT spectroscopy.";
RL Biochemistry 31:5237-5244(1992).
RN [12]
RP STRUCTURE BY NMR.
RX MEDLINE=94320651; PubMed=8045306;
RA Stockman B.J., Scahill T.A., Strakalaitis N.A., Brunner D.P.,
RA Yem A.W., Deibel M.R. Jr.;

```

"Solution structure of human interleukin-1 receptor antagonist protein."; 349:79-83(1994).

[13] X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=94230368; Pubmed=8175703;

RA Vigers G.P.A., Caffes P., Evans P., Thompson R.C., Eisenberg S.P., Brandhuber B.J.;

RA "X-ray structure of interleukin-1 receptor antagonist at 2.0-A resolution.";

RL J. Biol. Chem. 269:12874-12879(1994).

[14] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).

RX MEDLINE=95172072; Pubmed=7867645;

RA Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E., Akesson A., Bowlin T.L., Yanofsky S., Barrett R.W.;

RA "Refined crystal structure of the interleukin-1 receptor antagonist. Presence of a disulfide link and a cis-proline.";

RL Eur. J. Biochem. 227:838-847(1995).

[15] X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.

RX MEDLINE=97215904; Pubmed=9062194;

RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A., Sarubbi E., Akesson A., Bowlin T., Yanofsky S., Barrett R.W.;

RA "A new cytokine-receptor binding mode revealed by the crystal structure of the IL-1 receptor with an antagonist.";

RL Nature 386:194-200(1997).

CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.

CC -!- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR (ISOFORMS 2, 3 AND 4).

CC -!- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2/ilc1-lra, 3/ilc1-lra type II and 4; are produced by alternative splicing.

CC -!- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.

CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.

CC -!- DATABASE: NAME-R&D Systems' cytokine source book: IL1RN; WWW="http://www.rndsystems.com/asp/q\_sitebuilder.asp?bodyig=205".

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DR EMBL; M55646; AAA59138.1; -

DR EMBL; M63099; ABA1943.1; -

DR EMBL; X52015; CAA36262.1; -

DR EMBL; X53296; CAA37386.1; -

DR EMBL; X64532; CAA45632.1; -

DR EMBL; U65590; AAB92268.1; -

DR EMBL; U65590; AAB92270.1; -

DR EMBL; X84348; CAA59087.1; -

DR EMBL; U65590; AAB92269.1; -

DR EMBL; AF043143; AAC39672.1; -

DR PIR; A30368; A30368.

DR PIR; A37822; A37822.

DR PIR; S08160; S08160.

DR PIR; S08159; S08159.

DR PIR; A40956; A40956.

DR PIR; A39386; A39386.

DR PDB; 1ITN; 30-APR-94.

DR PDB; 2IRT; 15-OCT-94.

DR PDB; 1IRP; 27-FEB-95.

DR PDB; 1ILR; 07-FEB-95.

DR PDB; 1ILT; 01-APR-95.

DR PDB; 1IRA; 17-JUN-98.

DR Aarhus/Ghent-2DPAGE; 7104; IEF.

DR Aarhus/Ghent-2DPAGE; 7105; IEF.

DR MIM; 147679; -

DR InterPro; IPR000975; Interleukin\_1.

DR Pfam; PF00340; IL1; 1.

DR PRINTS; PRO0264; INTERLEUKIN1.

DR ProDom; PD002536; Interleukin\_1; 1.

DR SMART; SM00125; IL1; 1.

DR PROSITE; PS00253; INTERLEUKIN\_1; 1.

KW Glycoprotein; Signal; Alternative splicing; 3D-structure.

FT SIGNAL 1 25 INTERLEUKIN-1 RECEPTOR ANTAGONIST

FT CHAIN 26 177 PROTEIN.

FT DISULFID 91 141 N-LINKED (GLNAC... ) (POTENTIAL).

FT CARBOHYD 109 109 MEICRGLRSLITLLFLPHS -> MAL (IN

FT VARSPLIC 1 21 ISOFORM 2).

FT VARSPLIC 1 21 MEICRGLRSLITLLFLPHS -> MALADLYEEGGGGG

FT VARSPLIC 1 34 GEDNADSK (IN ISOFORM 3).

FT VARSPLIC 1 34 MISSING (IN ISOFORM 4).

SQ SEQUENCE 177 AA; 20055 MW; DI690776A7394057 CRC64;

Query Match 27.2%; Score 101; DB 1; Length 177;

Best Local Similarity 37.5%; Pred. No. 1.6e-05;

Matches 24; Conservative 8; Mismatches 26; Indels 6; Gaps 1;

QY 3 DIMDLYNQPEPVKSLFLYHSQSGRNSTPESVAFPGWFIASVSGGCPLLITQLGKANTT 62

Db 109 NITDLSNRKKDKRFARFIRSDSGPTTSPESAACPGFLCTAMEADQPVSLT-----NMP 162

QY 63 DFGL 66

Db 163 DEGV 166

RESULT 7

IL1B\_PIG STANDARD; PRT; 267 AA.

AC P26889;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Interleukin-1 beta precursor (IL-1 beta).

GN IL1B.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93314975; Pubmed=8325511;

RA Huether M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.;

RT "Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 beta.";

RL Gene 129:285-289(1993).

CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.

CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.

CC -!- SUBUNIT: MONOMER.

CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETORY PROTEINS.

CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M86725; AAA02584.1; -.
DR PIR; JN0724; JN0724.
DR HSSP; P01584; LHBF.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR000975; Interleukin_1.
DR InterPro; IPR003502; Interleukin_1_prop.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_HBGF.
DR PRINTS; PR00262; IL1_HBGF.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 114 BY SIMILARITY.
FT CHAIN 115 267 INTERLEUKIN-1 BETA.
SQ SEQUENCE 267 AA; 30404 MW; 7F6B92B784D5086F CRC64;

Query Match 25.9%; Score 96; DB 1; Length 267;
Best Local Similarity 30.6%; Pred. No. 0.00011;
Matches 19; Conservative 13; Mismatches 30; Indels 0; Gaps 0;

QY 8 YNQPVPKFLYHSGSRNSTFESVAPGWFIAVSSEGGCPILITQELGKANTDTFGLT 67
DB 204 YPRDMEKRFVYKTEIKNRVFEFSALEPNWYISTSAEQKPVFLGNSKGRQDITDTWE 263
QY 68 ML 69
DB 264 VL 265

RESULT 8
IL1X_BOVIN
ID IL1X_BOVIN STANDARD; PRT; 174 AA.
AC Q77482;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98305607; PubMed-9643454;
RA Kirisawa R., Fukuda T., Yamanaka H., Hagiwara K., Goto M., Obata Y.,
RA Yoshino T., Iwai H.;
RT "Enzymatic amplification and expression of bovine interleukin-1
RT receptor antagonist cDNA.";
RL Vet. Immunol. Immunopathol. 62:197-208(1998).
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB005148; BAA31854.1; -.
DR HSSP; P18510; IL1R.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
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DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 174 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 89 139 BY SIMILARITY.
FT CARBOHYD 107 107 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 174 AA; 19926 MW; 1E56E7F224FF851F CRC64;

Query Match 25.6%; Score 95; DB 1; Length 174;
Best Local Similarity 41.2%; Pred. No. 9.1e-05;
Matches 21; Conservative 6; Mismatches 24; Indels 0; Gaps 0;

QY 3 DIMDLYNQPEPVKFLYHSGSRNSTFESVAPGWFIAVSSEGGCPILIT 53
DB 107 NITDLNQNEQDKRFAFIRFDNGPTTSFESACPGWFLCTSLEADQPVGLT 157

RESULT 9
IL1B_SHEEP
ID IL1B_SHEEP STANDARD; PRT; 266 AA.
AC P21621;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN IL1B.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92119335; PubMed-1840515;
RA Seow H.F., Rothel J.S., David M.J., Wood P.R.;
RT "Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.";
RL DNA Seq. 1:423-426(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91088326; PubMed-2263490;
RA Fiskerstrand C., Sargan D.;
RT "Nucleotide sequence of ovine interleukin-1 beta.";
RL Nucleic Acids Res. 18:7165-7165(1990).
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: MONOMER.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X54796; CAA38566.1; -.
DR EMBL; X56972; CAA40293.1; -.
DR PIR; S13092; S13092.
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RESULT 10
-IL1B_CAPHI
ID IL1B_CAPHI STANDARD; PRT; 266 AA.
F79162;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
ID IL1B.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Takakura H., Hashimoto O., Mori Y., Tatsumi M.;
RT "Molecular cloning and expression of caprine IL-1alpha and
RL IL-1beta.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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RESULT 11
IL1B_CEREL
ID IL1B_CEREL STANDARD; PRT; 266 AA.
AC P51745;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN IL1B.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
[1]
RN SEQUENCE FROM N.A.
RA Lockhart E.A.;
RP Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RL
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION AND PROLIFERATION, AND FIBROBLAST GROWTH FACTOR
CC ACTIVITY. IL-1 IS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (BY similarity).
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS (By similarity).
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC
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RA Driscoll P.C., Gronenborn A.M., Wingfield P.T., Clore G.M.;  
 RT "Determination of the secondary structure and molecular topology of  
 RT interleukin-1 beta by use of two- and three-dimensional heteronuclear  
 RL 15N-1H NMR spectroscopy.";  
 RL Biochemistry 29:4668-4682(1990).  
 RN [16]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE-91159409; PubMed=2001363;  
 RA Clore G.M., Wingfield P.T., Gronenborn A.M.;  
 RT "High-resolution three-dimensional structure of interleukin 1 beta in  
 RT solution by three- and four-dimensional nuclear magnetic resonance  
 RT spectroscopy.";  
 RL Biochemistry 30:2315-2323(1991).  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS  
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
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 CC -----  
 DR EMBL; M15840; AAA71137.1; -;  
 DR EMBL; X02532; CAA26372.1; -;  
 DR EMBL; X02770; AAA36106.1; -;  
 DR EMBL; X04500; CAA28185.1; -;  
 DR EMBL; X56087; CAA39567.1; -;  
 DR EMBL; M54933; AAA59136.1; -;  
 DR EMBL; M15330; AAA59135.1; -;  
 DR EMBL; BC008678; AAH08678.1; -;  
 DR PIR; A01848; ICHUL1.  
 DR PIR; A25542; A25542.  
 DR PIR; A29019; A29019.  
 DR PIR; B27616; B27616.  
 DR PIR; S19826; S19826.  
 DR PDB; 1I1B; 15-OCT-92.  
 DR PDB; 2I1B; 15-JUL-93.  
 DR PDB; 4I1B; 15-JAN-93.  
 DR PDB; 5I1B; 15-OCT-94.  
 DR PDB; 6I1B; 15-OCT-92.  
 DR PDB; 7I1B; 15-OCT-92.  
 DR PDB; 2I1B; 15-APR-92.  
 DR PDB; 3I1B; 15-APR-92.  
 DR PDB; 4I1B; 15-JUL-92.  
 DR PDB; 1H1B; 31-JAN-94.  
 DR PDB; 1I0B; 17-AUG-96.  
 DR PDB; 1I1B; 04-FEB-98.  
 DR PDB; 9I1B; 06-JAN-99.  
 DR PDB; 147720; -;  
 DR InterPro; IPR002348; IL1\_HBGF.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR InterPro; IPR003502; Interleukin\_1\_prop.  
 DR Pfam; PF00340; IL1; 1.  
 DR Pfam; PF02394; IL1\_propep; 1.  
 DR PRINTS; PR00262; IL1HBGF.  
 DR ProDom; PD002536; Interleukin\_1; 1.  
 DR SMART; SM00125; IL1; 1.  
 DR SPORTE; PS00253; INTERLEUKIN\_1; 1.  
 DR Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;

KW 3D-structure. 1 116  
 FT PROPEP 117 269  
 FT CHAIN 6 6  
 FT CONFLICT 20 20  
 FT CONFLICT 111 111  
 FT CONFLICT 177 177  
 FT CONFLICT 214 214  
 FT STRAND 121 128  
 FT TURN 129 130  
 FT STRAND 132 138  
 Query Match 22.9%; Score 85; DB 1; Length 269;  
 Best Local Similarity 33.3%; Pred. No. 0.0027;  
 Matches 21; Conservative 8; Mismatches 32; Indels 2; Gaps 1;  
 QY 8 YNQPEPVKSFLLYHSGNSGNSFTFESVAPFGWFIASVSSEGGCLILITQELGKANTTDFGLT 67  
 DB 206 YPKKMEKREVFVNKINNKLEFESAQFPNVIYSTQAEINMPVFLGGTKGGQDITDF--T 263  
 QY 68 MLF 70  
 DB 264 MQF 266  
 RESULT 15  
 IL1B\_MACMU STANDARD; PRT; 269 AA.  
 AC P48090;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Interleukin-1 beta precursor (IL-1 beta).  
 GN IL1B.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE-96003435; PubMed=7561102;  
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;  
 RT "Comparative sequence analysis of cytokine genes from human and  
 RT nonhuman primates.";  
 RL J. Immunol. 155:3946-3954(1995).  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS  
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
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 CC -----  
 DR EMBL; U19845; AAA86709.1; -;  
 DR HSSP; P01584; 1H1B.  
 DR InterPro; IPR002348; IL1\_HBGF.

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DR InterPro; IPR000975; Interleukin_1.
DR InterPro; IPR003502; Interleukin_1_prop.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 116
FT CHAIN 117 269 INTERLEUKIN-1 BETA.
SQ SEQUENCE 269 AA; 30481 MW; A7CD59EBAC120EC7 CRC64;

Query Match 22.9%; Score 85; DB 1; Length 269;
Best Local Similarity 33.3%; Pred. No. 0.0027;
Matches 21; Conservative 8; Mismatches 32; Indels 2; Gaps 1;

QY 8 YNQPEPVKSFLEYHSQSGRNSTFSVAFPGWFIAYVSEGGGCPFLILTQELGRANTTDFGLT 67
Db 206 YPKKKMEKRFVINKIEINNKLEFESAQFPNWIYSTISQAENMPVFLGGTRGGQDITDF--T 263

QY 68 MLF 70
Db 264 MQF 266

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Search completed: June 20, 2002, 15:11:19  
 Job time: 444 sec



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OM protein - protein search, using sw model.

Run On: June 20, 2002, 15:03:09 ; Search time 61.16 seconds  
(without alignments)  
197.999 Million cell updates/sec

Title: US-09-763-498-6  
Perfect score: 371  
Sequence: 1 EKDIMLYNQPEPVKSFLEY.....ILTQELGKANTDFGLTMLF 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_rvirus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	371	100.0	158	4 Q9UHA7	Q9uha7 homo sapien
2	238	64.2	160	11 Q9JLA2	Q9jla2 mus musculus
3	208.5	56.2	169	4 Q9NZH8	Q9nzh8 homo sapien
4	184	49.6	157	4 Q9UHA5	Q9uha5 homo sapien
5	158	42.6	183	11 Q9D6Z6	Q9d6z6 mus musculus
6	127	34.2	155	11 Q9QYI1	Q9qyi1 mus musculus
7	127	34.2	156	11 Q9JIG2	Q9jig2 mus musculus
8	124	33.4	155	4 Q9UBH0	Q9ubh0 homo sapien
9	107	28.8	72	6 Q77771	Q77771 equus caball
10	101	27.2	159	4 Q96GD6	Q96gd6 homo sapien
11	101	27.2	177	6 Q9GMZ4	Q9gmz4 tursiops tr
12	98	26.4	176	6 Q9BEH0	Q9beh0 canis famil
13	97	26.1	144	4 Q9BXI1	Q9bxi1 homo sapien
14	97	26.1	152	4 Q969H5	Q969h5 homo sapien
15	96.5	26.0	283	13 Q9PVZ5	Q9pvz5 xenopus lae
16	96	25.9	267	6 Q29082	Q29082 sus scrofa

17	93.5	25.2	267	13	073909	073909 gallus gall
18	91	24.5	276	13	057398	057398 cyprinus ca
19	91	24.5	276	13	09PW18	09pw18 cyprinus ca
20	89	24.0	272	13	Q9DDF3	Q9ddf3 cyprinus ca
21	88	23.7	176	6	Q9GKK2	Q9gkk2 canis famil
22	87	23.5	272	13	Q9DDF2	Q9ddf2 cyprinus ca
23	86.5	23.3	178	4	Q9HBF2	Q9hbff2 cyprinus ca
24	86.5	23.3	192	4	Q9UHA6	Q9uha6 homo sapien
25	86.5	23.3	218	4	Q9NZH6	Q9nzh6 homo sapien
26	86.5	23.3	218	4	Q9HBF3	Q9hbff3 homo sapien
27	85	22.9	153	4	Q43645	Q43645 homo sapien
28	85	22.9	269	4	Q96HE5	Q96he5 homo sapien
29	83.5	22.5	261	13	Q9UWH4	Q9uwh4 dicentrarch
30	81	21.8	266	6	Q9TTK1	Q9ttk1 tursiops tr
31	79.5	21.4	253	13	Q9OW32	Q9ow32 sparus aura
32	73.5	19.8	260	13	Q9YGD3	Q9ygd3 oncorhynch
33	68.5	18.5	64	13	Q9SGS5	Q9sgs5 scophthalmu
34	66.5	17.9	267	11	Q9IZL5	Q9izl5 sigmodon hi
35	66.5	17.9	957	4	Q9URN0	Q9urn0 homo sapien
36	65.5	17.7	599	11	Q9IWP7	Q9iwp7 mus musculu
37	64.5	17.4	541	10	Q940N8	Q940n8 arabidopsis
38	64.5	17.4	541	10	Q93Z31	Q93z31 arabidopsis
39	64	17.3	357	2	Q93SK6	Q93sk6 myxococcus
40	63	17.0	364	16	P73423	P73423 synechocyst
41	62.5	16.8	148	15	Q9OM28	Q9om28 human immun
42	62.5	16.8	254	13	Q9PT12	Q9pt12 oncorhynch
43	62.5	16.8	533	5	017592	017592 caenorhabdi
44	62.5	16.8	1003	15	093086	093086 human immun
45	62	16.7	939	16	Q9KQC8	Q9kqc8 vibrio chol

## ALIGNMENTS

RESULT 1

Q9UHA7 PRELIMINARY: PRT; 158 AA.  
AC Q9UHA7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE FIL1 EPSILON.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Rominidae; Homo.  
OX NCBI\_taxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20092888; PubMed=10625660;  
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,  
RA Sims J.E.;  
RT "Four New Members Expand the IL-1 Superfamily.";  
RL J. Biol. Chem. 275:1169-1175(2000).  
DR EMBL; AF201831; AAF25211.1; .  
DR HSSP; P18510; ILIR.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
DR ProDom; PD002536; Interleukin\_1; 1.  
DR SMART; SM00125; IL1; 1.  
SQ SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;

Query Match 100.0%; Score 371; DB 4; Length 158;  
Best Local Similarity 100.0%; Pred. No. 2e-39;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKDIMLYNQPEPVKSFLEYHSQGRNSTFESVAPGWFIATVSSEGCPILITQELGKAN 60  
|||||

Db 89 EKDIMLYNQPEPVKSFLEYHSQGRNSTFESVAPGWFIATVSSEGCPILITQELGKAN 148  
|||||

QY 61 TTDFGLTMLF 70  
|||||

Db 149 TTDFGLTMLF 158

Query Match 64.2%; Score 238; DB 11; Length 160;  
Best Local Similarity 63.8%; Pred. No. 1.8e-22;  
Matches 44; Conservative 11; Mismatches 14; Indels 0; Gaps 0;  
QY 1 EKDIMDLYNQPEPVKSFILYHQSQRNSTFESVAFPGWFIIVSSEGCPILITQELGRAN 60

```

RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL: AF201833; AAF25213.1; -
DR HSSP: P10749; 2MIB.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ SEQUENCE 157 AA; 17702 MW; 7A54F3D7557A3EE3 CRC64;

Query Match 49.6%; Score 184; DB 4; Length 157;
Best Local Similarity 51.5%; Pred. No. 1.4e-15;
Matches 34; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 EKIDMLYNQPEPVKSFLEFHSQSGRNSTFESVAFPGWFIASVSGGCPPLITLQELGKAN 60
   ||:||||: | |||:|: | |||:||||| | : | : ||:| |
Db 88 EKINDLYVEKKAQKAPLFYHGIEGSTSVFQSVLPYPGWFIATSTSGQPIPLTREGITN 147
   ||:||||: | |||:|: | |||:||||| | : | : ||:| |
QY 61 TTDFGL 66
   |:||
Db 148 NTNFFL 153
   |:||

RESULT 5
Q9D626 PRELIMINARY; PRT; 183 AA.
AC Q9D626;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 2310043N2ORIK PROTEIN.
GN 2310043N2ORIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK009787; BAB26505.1; -
DR HSSP: P01584; 1H1B.
DR MGD: MGI:1916927; 2310043N2ORIK.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; UNKNOWN_1.

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SQ SEQUENCE 183 AA; 20878 MW; A3ACE339FB96F02F CRC64;

Query Match 42.6%; Score 158; DB 11; Length 183;
Best Local Similarity 50.0%; Pred. No. 3.4e-12;
Matches 32; Conservative 9; Mismatches 23; Indels 0; Gaps 0;

QY 1 EKIDMLYNQPEPVKSFLEFHSQSGRNSTFESVAFPGWFIASVSGGCPPLITLQELGKAN 60
   ||:||||: | |||:|: | |||:||||| | : | : ||:| |
Db 114 EVDIMNLYKKAQKAPLFYHGIEGSTSVFQSVLPYPGWFIATSTSGQPIPLTREGITN 173
   ||:||||: | |||:|: | |||:||||| | : | : ||:| |
QY 61 TTDF 64
   |:||
Db 174 NTNF 177
   |:||

RESULT 6
Q9QYI1 PRELIMINARY; PRT; 155 AA.
AC Q9QYI1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE IL-1L1 PROTEIN (INTERLEUKIN-1 HOMOLOG 3).
GN IL1F5 OR IL1H1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton J.L., Nicklin M.J.H.;
RT "IL-1L1: A Novel Member of the Interleukin-1 Gene Family is Expressed
   in Trophoblasts and Macrophages.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Trzimas M.N.,
RA Griswold D.E., Capper E.A., Tai-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
   the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
DR EMBL: AJ250429; CAB59831.1; -
DR EMBL: AF200495; AAF69251.1; -
DR HSSP: P18510; 1ILR.
DR MGD: MGI:1859325; IL1f5.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
SQ SEQUENCE 155 AA; 17004 MW; A4B1770F2E12533A CRC64;

Query Match 34.2%; Score 127; DB 11; Length 155;
Best Local Similarity 43.9%; Pred. No. 2.5e-08;
Matches 29; Conservative 7; Mismatches 26; Indels 4; Gaps 1;

QY 3 DIMDLYNQPEPVKSFLEFHSQSGRNSTFESVAFPGWFIASVSGGCPPLITQ----ELGK 58
   ||:||||: | |||:|: | |||:||||| | : | : ||:| |
Db 84 NMIELYLGAKSKSFYFRDMLGTLSTFESAIPGWFCLCTSPFADQPVRLTIQIPEDPAWD 143
   ||:||||: | |||:|: | |||:||||| | : | : ||:| |
QY 59 ANTTDF 64
   |:||
Db 144 APITDF 149
   |:||

RESULT 7
Q9JIG2 PRELIMINARY; PRT; 156 AA.
ID Q9JIG2
AC Q9JIG2;

```

DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE INTERLEUKIN-1 DELTA (INTERLEUKIN 1 RECEPTOR ANTAGONIST HOMOLOG 1)  
 DE IL1F5 OR IL1HL1  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,  
 RA Kastelein R.A.;  
 RT "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=TONGUE; AND STOMACH;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombaearts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AF230378; AAF91275.1; -;  
 DR EMBL: AK009741; BAB26471.1; -;  
 DR EMBL: AK008977; BAB26002.1; -;  
 DR HSSP: P18510; IL1R.  
 DR MGD: MGI:1859325; IL1F5.  
 DR InterPro: IPR000975; Interleukin\_1.  
 DR Pfam: PF00340; IL1; 1.  
 DR ProDom: PD002536; Interleukin\_1; 1.  
 DR SMART: SM00125; IL1; 1.  
 DR PROSITE: PS00253; INTERLEUKIN\_1;  
 SQ SEQUENCE 156 AA; I7136 MW; A4D1EE2F93CF77A7 CRC64;

Query Match 34.2%; Score 127; DB 11; Length 156;  
 Best Local Similarity 43.9%; Pred. No. 2.5e-08;  
 Matches 29; Conservative 7; Mismatches 26; Indels 4; Gaps 1;  
 1;

Qy 3 DIMDLYNQPEPVKSFLEFVHQSQRNSTFESVAPPGWFIASVSGGCPILITQ----ELGK 58  
 Db 85 NIMELYLGAKESKSFTEYFRDMDGLTSSFESAAYPGWFLCTSPADQPVRLTQIPEDPAWD 144

Qy 59 ANTTDF 64  
 Db 145 APITDF 150

RESULT 8  
 Q9UBH0 PRELIMINARY; PRT; 155 AA.  
 AC Q9UBH0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)

DE FILI DELTA (INTERLEUKIN-1 LIKE PROTEIN 1) (INTERLEUKIN-1 RECEPTOR  
 DE ANTAGONIST HOMOLOG 1) (INTERLEUKIN-1 DELTA).  
 GN IL1HL1 OR IL1L1  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20092888; PubMed=10625660;  
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,  
 RA Sims J.E.;  
 RT "Four New Members Expand the IL-1 Superfamily.";  
 RL J. Biol. Chem. 275:1169-1175(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99443727; PubMed=10512743;  
 RA Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,  
 RA Drmanac R., Ford J.E.;  
 RT "IL1Y1: A Novel Interleukin-1 Receptor Antagonist Gene.";  
 RL Biochem. Biophys. Res. Commun. 263:702-706(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RA Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.;  
 RT "A tissue specific interleukin-1 receptor antagonist homolog from the  
 RT IL1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Barton J.L., Herbst R., Bosisio D., Nicklin M.J.H.;  
 RT "A tissue specific interleukin-1 receptor antagonist homolog from the  
 RT IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20322477; PubMed=10866108;  
 RA Mulero J.J., Nelken S.T., Ford J.E.;  
 RT "Organization of the Human Interleukin-1 Receptor Antagonist Gene  
 RT IL1HL1.";  
 RL Immunogenetics 51:425-428(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,  
 RA Kastelein R.A.;  
 RT "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF201830; AAF25210.1; -;  
 DR EMBL: AF186094; AAF02757.1; -;  
 DR EMBL: AJ242737; CAB59822.1; -;  
 DR EMBL: AJ242738; CAB59823.1; -;  
 DR EMBL: AJ271338; CAB67704.1; -;  
 DR EMBL: AF216693; AAF76981.1; -;  
 DR EMBL: AF230377; AAF91274.1; -;  
 DR HSSP: P18510; IL1R.  
 DR InterPro: IPR000975; Interleukin\_1.  
 DR Pfam: PF00340; IL1; 1.  
 DR ProDom: PD002536; Interleukin\_1; 1.  
 DR SMART: SM00125; IL1; 1.  
 DR PROSITE: PS00253; INTERLEUKIN\_1; UNKNOWN\_1.  
 KW Receptor.  
 SQ SEQUENCE 155 AA; 16962 MW; B96DB5EFA2612E25 CRC64;

Query Match 33.48; Score 124; DB 4; Length 155;  
 Best Local Similarity 45.5%; Pred. No. 6e-08;  
 Matches 30; Conservative 7; Mismatches 25; Indels 4; Gaps 2;  
 2;

Qy 3 DIMDLYNQPEPVKSFLEFVHQSQRNSTFESVAPPGWFIASVSGGCPILITQ--ELG--K 58  
 Db 84 NIMELYLGAKESKSFTEYFRDMDGLTSSFESAAYPGWFLCTVPADQPVRLTQIPENGWNN 143

Qy 59 ANTTDF 64

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Db      144  APITDF 149

RESULT  9
O77771  PRELIMINARY; PRT; 72 AA.
AC O77771;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST SECRETORY FORM (FRAGMENT).
GN IL-1RA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BREED THOROUGHbred;
RA Dhar A.K., Thompson M.S., Paradis M.R., Alciivar-Warren A.;
RT "Molecular Characterization of Equine Interleukin 1 Receptor
   Antagonist (IL-1ra) Gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF072476; AAC62237.1; -.
DR HSSP; P18510; 1IRA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 72 AA; 8215 MW; 290CC9B9D4C413D9 CRC64;

Query Match 28.8%; Score 107; DB 6; Length 72;
Best Local Similarity 41.5%; Pred. No. 3.6e-06;
Matches 22; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

QY 3 DTMDLYNQPEPVKSFLEFVHSGRSTFESVAFPGWFIASVSGGCPILLTQE 55
Db 4 NITDLSENKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAQADRPVSLTK 56

RESULT 10
Q96GD6 PRELIMINARY; PRT; 159 AA.
AC Q96GD6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PANCREATIC ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC009745; AAH09745.1; -.
KW Receptor.
SQ SEQUENCE 159 AA; 17888 MW; C1D66CDF0D2F7B44 CRC64;

Query Match 27.2%; Score 101; DB 4; Length 159;
Best Local Similarity 37.5%; Pred. No. 5.3e-05;
Matches 24; Conservative 8; Mismatches 26; Indels 6; Gaps 1;

QY 3 DIMDLYNQPEPVKSFLEFVHSGRSTFESVAFPGWFIASVSGGCPILLTQELGKANTT 62

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Db      91  NITDLSENKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAQADRPVSLT-----NMP 144
QY      63  DFGL 66
Db      145  DEGV 148

RESULT 11
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ID Q9GMZ4;
AC Q9GMZ4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST.
GN IL-1RA.
OS Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21109087; PubMed=11182153;
RA Inoue Y., Ito T., Jimbo T., Syouji Y., Ueda K., Sakai T.;
RT "Molecular cloning and functional expression of bottle-nosed dolphin
   (Tursiops truncatus) interleukin-1 receptor antagonist.";
RL Vet. Immunol. Immunopathol. 78:131-141(2001).
DR EMBL; AB038268; BAB11806.1; -.
DR HSSP; P18510; 1IRA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Receptor.
SQ SEQUENCE 177 AA; 19923 MW; 6FD19A06C09B131B CRC64;

Query Match 27.2%; Score 101; DB 6; Length 177;
Best Local Similarity 43.1%; Pred. No. 5.9e-05;
Matches 22; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 3 DIMDLYNQPEPVKSFLEFVHSGRSTFESVAFPGWFIASVSGGCPILLT 53
Db 109 NITDLNSKEDKRAFIRSDSGPTTSFESAACPGWFLCTALETDPVGLT 159

RESULT 12
Q9BEH0 PRELIMINARY; PRT; 176 AA.
ID Q9BEH0;
AC Q9BEH0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin I.-S., Youn H.-Y.;
RT "Molecular cloning of canine interleukin-1 receptor antagonist (IL-
   1ra).";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY026462; AAK01472.1; -.
DR HSSP; P18510; 1ILR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 11:09:00 ; Search time 2828.95 seconds  
(without alignments)  
2275.773 Million cell updates/sec

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Perfect score: 477  
Sequence: 1 atggaaaagcattgaaat.....ggttaactatgctgttttaa 477

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674877542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estnu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_gss:\*
- 13: em\_gss\_hum:\*
- 14: em\_gss\_inv:\*
- 15: em\_gss\_pln:\*
- 16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	129.2	27.1	479	9	AA030324	AA030324 mi08c10.r
C 3	124.4	26.1	612	10	BM386666	BM386666 UI-R-CMI-
C 4	122	25.6	539	9	AW368430	AW368430 CM3-HT019
5	122	25.6	555	9	AW361172	AW361172 RC1-CT025
C 6	122	25.6	557	9	AW368437	AW368437 CM3-HT019
C 7	122	25.6	559	9	AW578451	AW578451 RC1-CT025
C 8	121	25.4	555	10	BE695960	BE695960 RC1-CT025
9	120.4	25.2	436	9	AW361164	AW361164 RC1-CT025
10	120.4	25.2	536	9	AW853610	AW853610 RC1-CT025
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12	113.2	23.7	870	10	BF244205	BF244205 601863146
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20	70.8	14.8	635	9	AW262191	AW262191 xq62f01.x
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22	70.8	14.8	910	9	AL549965	AL549965 AL549965
23	70.8	14.8	938	10	BE563703	BE563703 601335323
24	70.8	14.8	955	10	BM009048	BM009048 603618892
25	69.2	14.5	640	10	BG288796	BG288796 602388126
26	69.2	14.5	864	10	BI489807	BI489807 603031536
C 27	67.6	14.2	371	10	BI020838	BI020838 CM4-MT021
28	67.6	14.2	549	10	BE706905	BE706905 OVO-HT036
29	65.6	13.8	508	9	AW464284	AW464284 BP2300154
30	65	13.6	531	9	AW951593	AW951593 EST363663
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32	62	13.0	832	10	BI517352	BI517352 603041588
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35	61.2	12.8	1051	11	AK009741	AK009741 Mus muscu
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#### ALIGNMENTS

RESULT	AK004061	AK004061	883 bp	mRNA	linear	HTC 19-JAN-2002
LOCUS	Mus musculus	Mus musculus	18 days embryo	whole body	cDNA, RIKEN full-length	
DEFINITION	enriched library, clone:ll10033G16:interleukin 1 family, member 6 (epsilon), full insert sequence.					
ACCESSION	AK004061					
VERSION	AK004061.1	GI:12835089				
KEYWORDS	HTC; CAP trapper.					
SOURCE	Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA, clone:ll10033G16:interleukin 1 family, member 6 (epsilon), full insert sequence.					
ORGANISM	-Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
AUTHORS	1 (sites)					
TITLE	Carninci, P. and Hayashizaki, Y.					
JOURNAL	High-efficiency full-length cDNA cloning					
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)					
PUBMED	99279253					
REFERENCE	10349636					
AUTHORS	2 (sites)					
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.					
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes					
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)					
PUBMED	20499374					
REFERENCE	11042159					
AUTHORS	3 (sites)					
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.					
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer					
PUBMED	Genome Res. 10 (11), 1757-1771 (2000)					

MEDLINE	20530913
PUBMED	11076861
REFERENCE	4 (sites)
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5 (bases 1 to 883)
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojiima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,Y., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Ouackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,K., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Soabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohana Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site ( <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a> ) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGACGAGAGCGCCGAATTCAGTCTTTTGTGGTATTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGACGAGAGAGTCAAGAGCTCAATTAAATTAACCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.
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 VERSION AW3611172.1 GI:6865822  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 555)  
 AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.  
 TITLE The FAPESP/LICR Human Cancer Genome Project  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0251-141099-012-h04&t3=1999-10-14&t4=1>)  
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 BASE COUNT 148 a 129 c 130 g 147 t 1 others

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RESULT 6  
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 DEFINITION CM3-HT0192-071099-022-h06 HT0192 Homo sapiens cDNA, mRNA sequence.

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 VERSION AW368437.1 GI:6873087  
 KEYWORDS EST.  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 557)  
 AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.  
 TITLE The FAPESP/LICR Human Cancer Genome Project  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-HT0192-071099-022-h06&t3=1999-10-07&t4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence start: 43  
 High quality sequence stop: 557.

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 BASE COUNT 149 a 130 c 130 g 147 t 1 others

Query Match 25.6%; Score 122; DB 9; Length 557;  
 Best Local Similarity 71.9%; Pred. No. 1e-25;  
 Matches 174; Conservative 0; Mismatches 65; Indels 3; Gaps 1;  
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RESULT 7  
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VERSION ANS78451.1 GI:7253500
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SOURCE Homo sapiens
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLES 1 (bases 1 to 559)
JOURNAL HCGP http://www.ludwig.org.br/ORESTES..
COMMENT The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax.: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0252-
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Seq primer: puc 18 forward
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    from ORESTES PCR (U.S. Letters Patent application No. 196
    ,716 - Ludwig Institute for Cancer Research) profiles
    into the pUC 18 vector. Reverse transcription of tissue
    mRNA and cDNA amplification were performed under low
    stringency conditions."
BASE COUNT      148 a   130 c   132 g   149 t
ORIGIN
Query Match      25.68; Score 122; DB 9; Length 559;
Best Local Similarity 71.9%; Pred. NO. 1.le-25;
Matches 174; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

Qy 226  tgtgtaaagtgcgggaccagccacactcagctgaaggaaaagatataatgatattg 285
      ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 556  TGTGAGAAGTTGGAGAACACGCCACATTCAGCTAAAGAGCAGAAGATCATGTGATCTG 497
      ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

Qy 286  tacacaaccaaccgagctgtgaaagtccttctctttctaccacgccagagtgcgaggaac 345
      ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 496  TAGFGCAACCAGCCGCGTGAAACCTCTCTTTTACCGTCCAAGACTGGTAGGACC 437
      ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

Qy 346  tcacacctcgactgttgctgttcccctggctggctgcgtgcgtcagctctcaaggaggcc 405
      ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 436  TCCACCCTTGATCTGTGGCCTTCCCGGACTTGTTAT---TGCCTCCCTCCAAGAGAC 380
      ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

Qy 406  tgtcctctcatcttacccaagaactggggaagaccaaactactgacttgtgggttaact 465
      ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 379  CAGCCCATCATTTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCCTTGACTTAAT 320
      ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

Qy 466 at 467
      ||
Db 319 AT 318

RESULT 8
BE695960/c LOCUS BE695960
DEFINITION RC1-CT0252-150600-028-h05 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE695960
VERSION BE695960.1 GI:10083120

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Db 492 TCACCTTCTGCTCTTTTCAGTCAGTCCTCTATCTGCTGGTGTATATAGCCACCTCTTCCATA 551
Qy 400 ggaggctgcctctcatctctaccagaactcggggaagcaacacactactgactt 455
Db 552 GAAAGACAGACAATCATCCTCACATCATCAGCGGGGTAATGGTTTAACACTAACTT 607

RESULT 12
BF244205
LOCUS BF244205 870 bp mRNA linear EST 14-NOV-2000
DEFINITION 601863146F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080899 5',
mRNA sequence.
ACCESSION BF244205
VERSION BF244205.1 GI:11158135
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM941 row: k column: 12
High quality sequence stop: 582.
FEATURES
source
location/Qualifiers
1..870
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4080899"
/clone_lib="NIH_MGC_57"
/tissue_type="glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgccc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGGCGCCGACATG-3' (30)BN-3'
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 256 a 216 c 171 g 227 t
ORIGIN

Query Match 23.7%; Score 113.2; DB 10; Length 870;
Best Local Similarity 58.2%; Pred. No. 5.7e-23;
Matches 199; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

Qy 136 ttaatctcatccgacatgttgagacccttgagaaagacagagggaaaccccatcactg 195
Db 5 TTAATAGCCTCTAGAGACACAGATTCAGTCAGCAAGAAAGGTTATATGGTTTACTCTG 64

Qy 196 ggcctgaatggaactcaatctcgtcgtgatgtgtctaaagtgcggggaccagccacactc 255
Db 65 GGAATCAAGGGAAGAAAGATCTCTGCTCTCTGTCAGAAATTCAGGCAAGCCTACTTTG 124

Qy 256 cagctgaaggaaaggaataatgattgtacacccaacccagcgtctgaagtccttt 315
Db 125 CAGCTTAAGGAAAAAATATCATGACCTGTATGTGGAGAAGAAAGACAGAGAGCCCTTT 184

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Qy 316 ctctttaccacacaccagagtggcaggaactccacccttcagctgtggtttcccttgc 375
Db 185 CTTCTTTTCCACAATAAAGAAGGCTCCACTTCTGCTCTTTCAGTCAGTCCTTACCTGGC 244
Qy 376 tgggtcatcgtctgcagctctgaaggagctgctctctcatcttacccttaccgaactggg 435
Db 245 TGGTTCATAGCCACCTCCACCACATCAGGACGCCCATCTTTCACCAAGAGAGAGGC 304
Qy 436 aaagcccaactactgactgtgggttaactatgctgttttaa 477
Db 305 ATAATAACACATAACTTCTACTTAGATTCTGTGGAATAA 346

RESULT 13
AW753217/c
LOCUS AW753217 434 bp mRNA linear EST 28-APR-2000
DEFINITION RC1-CT0251-081099-011-a04 CT0251 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW753217
VERSION AW753217.1 GI:7668149
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0251-
081099-011-a04&t3=1999-10-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 42
High quality sequence stop: 67.
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location/Qualifiers
1..434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0251"
/dev_stage="Adult"
/notes="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 125 a 94 c 101 g 114 t
ORIGIN

Query Match 23.3%; Score 111; DB 9; Length 434;
Best Local Similarity 71.6%; Pred. No. 1.8e-22;
Matches 174; Conservative 0; Mismatches 65; Indels 4; Gaps 2;

Qy 226 tlgctaaagtgcgggaccagccacactgcagctgaagaaagata-taatggattt 284

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[illegible]

RESULT	14
AW361245	
LOCUS	560 bp mRNA linear EST 04-FEB-2000
DEFINITION	RC1-CT0252-181299-022-e08 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION	AW361245
VERSION	AW361245.1 GI:6865895
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 560) HCGP <a href="http://www.ludwig.org.br/ORESTES">http://www.ludwig.org.br/ORESTES</a> . The FAPESP/LICR Human Cancer Genome Project Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
AUTHORS	Tel: +55-11-2704922
TITLE	Fax: +55-11-2707001
JOURNAL	
COMMENT	

Email:	asimpson@ludwig.org.br
This sequence was derived from	the FAPESP/LICR Human Cancer Genome Project.
This entry can be seen in the following URL	(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCI6tS=RCI-Cr0252-181299-022-e086t3-1999-12-18&t4=1)
Seq primer:	puc 18 forward
High quality sequence start:	13
High quality sequence stop:	551.
Location/Qualifiers	
1..560	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone_lib="CT0252"	
/dev_stage="Adult"	
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	
143 a	131 c 141 g 145 t
BASE COUNT	
ORIGIN	

Query Match	20.4%	Score 97.4	DB 9	Length 560
Best Local Similarity	65.4%	pred. No. 2.5e-18		
Matches 159	Conservative	0	Mismatches 81	Indels 3
Gaps 1				

D <sub>b</sub>	21	GTATGTCAGAGGTTGGACCAAGCCCATATGCCAGCTCAGAGCAGCAGCATCGTGATCT	80
Q <sub>y</sub>	285	gtacaacaaaccggagcctgtgaagtcccttctctctaccacgccaagadtgccaggaa	344
D <sub>b</sub>	81	GTATGGACAACCAGAGCCCGTGAACCGCTTCTTGTCTACCGGGCCAAGACTGGTAGGAC	140
Q <sub>y</sub>	345	ctcaaccttcgagctctgtggctttcccctggctggttcatcgctctgcagctctgaagagg	404
D <sub>b</sub>	141	CTCCACCCCTTCAGTCTGTGGCTTTCGGGACTGGTTCATCGC---CTCCTCCAAAGAGAGA	197
Q <sub>y</sub>	405	ctgtcctctcatccttacccaagaactcggggaaagccaactactgactcttgggttaac	464
D <sub>b</sub>	198	CCAGCCCATCATCTGACTTCAGAACTCGGGAAGTCATAACAACACTGCCTTTGAATTAAA	257
Q <sub>y</sub>	465	tat	467
D <sub>b</sub>	258	TAT	260

RESULT	15
BG245180	
LOCUS	602357579f1 NCI_CGAP_Mam1 Mus musculus cdna clone IMAGE:4486098 5', linear EST 13-FEB-2001
DEFINITION	mRNA sequence.
ACCESSION	BG245180
VERSION	BG245180
KEYWORDS	BG245180.1 GI:12754995
SOURCE	EST.
ORGANISM	house mouse. Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 1020)
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: rcapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

FEATURES	source
Location/Qualifiers	
1. .1020	
/organism="Mus musculus"	
/strain="FVB/N"	
/db_xref="taxon:10090"	
/clone="IMAGE:4486098"	
/clone_lib="NCI-CCAP_Mam1"	
/tissue_type="tumor, biopsy sample"	
/dev_stage="10 months, virgin"	
/lab_host="DH10B"	
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"	
BASE COUNT	282 a 269 c 268 g 201 t
ORIGIN	

	Query Match	15.7%	Score 74.8;	DB 10;	Length 1020;
	Best Local Similarity	55.9%;	Pred. No. 2e-11;		
	Matches 142; Conservative	0; Mismatches 112;	Indels 0;	Gaps 0;	
Qy	188	tctactgggacctgaatgaactcaattcttcgtctgatgtgtcctaagtcggggaccacgc	247		
pb	268	tcttttttttggccatctcacggggccaccttgctctctcttttttgcctaaagtctcgagatgata	347		

Search completed: June 21, 2002, 11:09:01  
Job time: 17649 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:03:07 ; Search time 73.84 Seconds  
(without alignments)  
237,671 Million cell updates/sec

Title: US-09-763-498-8

Perfect score: 830  
Sequence: 1 MEKALKIDTPQGSIQDINH.....ILFQELGKANTDFGLTMLF 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
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22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	830	100.0	158	21	AA1980.DAT
2	826	99.5	158	21	AA1981.DAT
3	802	96.6	273	22	AA1982.DAT
4	646	77.8	130	22	AA1983.DAT
5	466.5	56.2	169	19	AA1984.DAT
6	466.5	56.2	169	20	AA1985.DAT
7	466.5	56.2	169	20	AA1986.DAT
8	466.5	56.2	169	22	AA1987.DAT
9	466.5	56.2	169	22	AA1988.DAT
10	466.5	56.2	173	22	AA1989.DAT
11	466.5	56.2	208	20	AA1990.DAT

Result No.	Score	Match	Length	ID	Description
12	463	55.8	157	22	AA1991.DAT
13	463	55.8	160	19	AA1992.DAT
14	463	55.8	160	20	AA1993.DAT
15	459.5	55.4	172	22	AA1994.DAT
16	459.5	55.4	172	22	AA1995.DAT
17	390	47.0	170	22	AA1996.DAT
18	385	46.4	157	22	AA1997.DAT
19	385	46.4	157	22	AA1998.DAT
20	371	44.7	70	21	AA1999.DAT
21	367.5	44.3	134	21	AA2000.DAT
22	367.5	44.3	134	21	AA2001.DAT
23	244.5	29.5	98	20	AA2002.DAT
24	239	28.8	72	19	AA2003.DAT
25	213	25.7	218	21	AA2004.DAT
26	210	25.3	176	22	AA2005.DAT
27	209	25.2	163	21	AA2006.DAT
28	209	25.2	167	21	AA2007.DAT
29	209	25.2	192	21	AA2008.DAT
30	209	25.2	193	21	AA2009.DAT
31	209	25.2	193	22	AA2010.DAT
32	209	25.2	197	21	AA2011.DAT
33	209	25.2	198	22	AA2012.DAT
34	209	25.2	203	21	AA2013.DAT
35	209	25.2	207	21	AA2014.DAT
36	209	25.2	218	21	AA2015.DAT
37	209	25.2	218	21	AA2016.DAT
38	209	25.2	218	21	AA2017.DAT
39	209	25.2	218	21	AA2018.DAT
40	209	25.2	218	21	AA2019.DAT
41	209	25.2	218	22	AA2020.DAT
42	209	25.2	218	22	AA2021.DAT
43	209	25.2	218	22	AA2022.DAT
44	207	24.9	218	21	AA2023.DAT
45	204	24.6	218	21	AA2024.DAT

#### ALIGNMENTS

RESULT 1  
AA1980.DAT 158 AA.  
ID AA1980.DAT 158 AA.  
AC AA1980.DAT 158 AA.  
DT 06-JUN-2000 (first entry)  
XX Human Interleukin-1 epsilon protein.  
DE Human Interleukin-1 epsilon protein.  
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
KW immunosuppressant; antirheumatic; antithrombotic; antipsoriatic;  
KW gene mapping; immune system; treatment; inflammatory disease;  
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
KW psoriasis; human.  
XX Homo sapiens.  
XX WO200011174-A1.  
XX 02-MAR-2000.  
XX 20-AUG-1999; 99WO-US18771.  
XX 21-AUG-1998; 98US-0097413.  
XX 31-AUG-1998; 98US-0098595.  
XX 11-SEP-1998; 98US-0099974.  
XX (IMV ) IMMUNEX CORP.  
XX Sins JE, Smith DE;  
XX WPI; 2000-237653/20.  
XX N-PSDB; AA251247.

Mouse interleukin-  
Rodent interleukin-  
Amino acid sequenc  
Human novel secret  
Human gene 13 enco  
Human interleukin-  
Human interleukin-  
Human IL-1 eta. H  
Partial human inte  
A novel polypeptid  
Human IL-1 recepto  
Amino acid sequenc  
Rodent interleukin  
Human zilla4-E200D  
Human extracellula  
Human IL-1 recepto  
Human IL-1 recepto  
Human interleukin-  
Processed human IL  
Human PRO3435. Ho  
Human interleukin-  
Interleukin-1 homo  
Human IL-1R1a fuse  
Human IL-1 recepto  
Human interleukin-  
Human IL-1 recepto  
Human zilla4 prote  
Human interleukin-  
Primate interleuki  
Human interleukin  
Interleukin-1 homo  
IL-1 related polyp  
Human zilla4-E200K  
Primate interleuki

XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
PT treat inflammatory and immune system-related diseases such as  
PT rheumatoid arthritis and inflammatory bowel disease -  
XX Claim 1b; Fig 2; 76pp; English.  
XX The present sequence is that of human Interleukin-1 (IL-1) epsilon  
CC protein. IL-1 epsilon gene is mapped to chromosome 2q and is mainly  
CC expressed in spleen, lymph node, thymus, tonsil and leucocyte  
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,  
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic  
CC activity. It can be used in the treatment of inflammatory or autoimmune  
CC diseases such as rheumatoid arthritis, inflammatory bowel disease and  
CC psoriasis. The DNA sequence can be used in chromosome identification,  
CC gene mapping and study of immune system.  
XX SQ Sequence 158 AA;  
Query Match 100.0%; Score 830; DB 21; Length 158;  
Best Local Similarity 100.0%; Pred. No. 1e-80;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEKALKIDTPQOGSIODINHRVWVLDQTLIAVPRKDRMSPTIALISCRHVETLEKDRG 60  
Db 1 MEKALKIDTPQOGSIODINHRVWVLDQTLIAVPRKDRMSPTIALISCRHVETLEKDRG 60  
Qy 61 NPVYLGNGNLCLMCAKVGDPDTLQLEKIDMDLYNQPEPVKSFLYHSQSGRNSTFES 120  
Db 61 NPVYLGNGNLCLMCAKVGDPDTLQLEKIDMDLYNQPEPVKSFLYHSQSGRNSTFES 120  
Qy 121 VAFPGWFIASVSEGGCPILITQELGKANTDFGLTMLF 158  
Db 121 VAFPGWFIASVSEGGCPILITQELGKANTDFGLTMLF 158  
RESULT 2  
AAV70218  
ID AAV70218 standard; Protein; 158 AA.  
XX AC AAV70218;  
XX DT 06-JUN-2000 (first entry)  
XX DE Human Interleukin-1 epsilon polymorphic variant.  
XX DE Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;  
KW gene mapping; immune system; treatment; inflammatory disease;  
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
KW psoriasis; polymorphic variant; human.  
XX OS Homo sapiens.  
XX FH Location/Qualifiers  
FT Key  
FT Misc-difference 12 /note= "Wild type Gln replaced with Arg"  
FT FT  
FN WO200011174-A1.  
XX PD 02-MAR-2000.  
XX PF 20-AUG-1999; 99WO-US18771.  
XX PR 21-AUG-1998; 98US-0097413.  
XX PR 31-AUG-1998; 98US-0098595.  
XX PR 11-SEP-1998; 98US-0099974.  
XX PA (IMMV ) IMMUNEX CORP.  
XX PI Sims JE, Smith DE;  
XX XX

DR WPI: 2000-237653/20.  
DR N-PSDB; AA251248.  
XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
PT treat inflammatory and immune system-related diseases such as  
PT rheumatoid arthritis and inflammatory bowel disease -  
XX Claim 1b; Fig 2; 76pp; English.  
XX The present protein sequence is that of human Interleukin-1 (IL-1)  
CC epsilon polymorphic variant. IL-1 epsilon gene is mapped to chromosome 2q  
CC and is mainly expressed in spleen, lymph node, thymus, tonsil and  
CC leucocyte tissues. IL-1 epsilon is a cytokine, with antiinflammatory,  
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic  
CC activity. It can be used in the treatment of inflammatory or autoimmune  
CC diseases such as rheumatoid arthritis, inflammatory bowel disease and  
CC psoriasis. The DNA sequence can be used in chromosome identification,  
CC gene mapping and study of immune system.  
XX SQ Sequence 158 AA;  
Query Match 99.5%; Score 826; DB 21; Length 158;  
Best Local Similarity 99.4%; Pred. No. 2.7e-80;  
Matches 157; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEKALKIDTPQOGSIODINHRVWVLDQTLIAVPRKDRMSPTIALISCRHVETLEKDRG 60  
Db 1 MEKALKIDTPQOGSIODINHRVWVLDQTLIAVPRKDRMSPTIALISCRHVETLEKDRG 60  
Qy 61 NPVYLGNGNLCLMCAKVGDPDTLQLEKIDMDLYNQPEPVKSFLYHSQSGRNSTFES 120  
Db 61 NPVYLGNGNLCLMCAKVGDPDTLQLEKIDMDLYNQPEPVKSFLYHSQSGRNSTFES 120  
Qy 121 VAFPGWFIASVSEGGCPILITQELGKANTDFGLTMLF 158  
Db 121 VAFPGWFIASVSEGGCPILITQELGKANTDFGLTMLF 158  
RESULT 3  
AAE03417  
ID AAE03417 standard; Protein; 273 AA.  
XX AC AAE03417;  
XX DT 03-AUG-2001 (first entry)  
XX DE Human interleukin-1 receptor antagonist-like (IL-lra-L).  
XX DE Human; interleukin-1 receptor antagonist-like protein; IL-lra-L; therapy;  
KW rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;  
KW joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;  
KW transplant rejection; graft versus host disease; strain; sprain; leprosy;  
KW cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;  
KW clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;  
KW myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;  
KW acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;  
KW eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;  
KW hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;  
KW infertility; endometriosis; retinal neuropathy; acute pancreatitis;  
KW Kawasaki's disease; cancer.  
XX OS Homo sapiens.  
XX PN WO200141792-A1.  
XX PD 14-JUN-2001.  
XX PF 04-DEC-2000; 2000WO-US32891.  
XX PR 10-DEC-1999; 99US-0170105.  
XX PR 28-NOV-2000; 2000US-0724859.  
XX XX

PA (AMGE-) AMGEN INC.  
 XX Calzone FJ, Luethy R, Boedigheimer MJ, Zhu J, Chung Y, Jing S;  
 PI WPI; 2001-381495/40.  
 XX N-PSDB; AAD06911.  
 DR  
 XX  
 PT Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the  
 PT polypeptide encoded by the nucleic acid is useful diagnosis, treatment,  
 PT and prevention of diseases such as arthritis, diabetes, transplant  
 PT rejection  
 XX  
 PS Claim 13; Fig 1A; 127pp; English.  
 XX  
 CC The present sequence is human interleukin-1 receptor antagonist-like  
 CC (IL-1ra-L) protein. IL-1ra-L is useful for treating, preventing or  
 CC ameliorating IL-1ra-L polypeptide-related disease, condition or disorder  
 CC which include rheumatoid arthritis, psoriatic arthritis, inflammatory  
 CC arthritis, osteoarthritis, autoimmune disease, multiple sclerosis, graft  
 CC lupus, diabetes, transplant rejection, inflammatory joint disease, graft  
 CC versus host disease and inflammatory conditions resulting from strain,  
 CC sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human  
 CC immunodeficiency virus (HIV) infection, clostridium-associated  
 CC diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,  
 CC anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory  
 CC disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,  
 CC psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,  
 CC Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,  
 CC lymphomas, lung and breast cancer, leukaemias, infertility,  
 CC endometriosis, retinal degeneration, retinal neuropathy, acute  
 CC pancreatitis and Kawasaki's disease.  
 XX  
 SQ Sequence 273 AA;  
 Query Match 96.6%; Score 802; DB 22; Length 273;  
 Best Local Similarity 98.7%; Pred. No. 2e-77;  
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LKIDTPQGGSIQIDINHRVWVLDQTLIAVPRKDRMSPTIALISCRHVETLEKGRNPIY 64  
 DB 120 LKIDTPQGGSIQIDINHRVWVLDQTLIAVPRKDRMSPTIALISCRHVETLEKGRNPIY 179  
 QY 65 LGLNGLNCLMCAKVGDDPTLQLKEKDINDLYNOPEPVKSFLEYHSQSGRNSTFESVAFP 124  
 DB 180 LGLNGLNCLMCAKVGDDPTLQLKEKDINDLYNOPEPVKSFLEYHSQSGRNSTFESVAFP 239  
 QY 125 GWFIVASSEGCPILITQELGKANTTDFGLTMLF 158  
 DB 240 GWFIVASSEGCPILITQELGKANTTDFGLTMLF 273  
 RESULT 4  
 ID AAB85001 standard; Protein; 130 AA.  
 XX  
 AC AAB85001;  
 XX  
 DT 06-AUG-2001 (first entry)  
 XX  
 DE Human interleukin-1 receptor antagonist (NOVINTRA C) polypeptide.  
 XX  
 KW NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;  
 KW gonadotropin-like protein; NOVAGON; interleukin-1; NOVINTRA; human;  
 KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;  
 KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;  
 KW antiasthmatic; antiallergic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200140291-A2.  
 XX  
 PD 07-JUN-2001.

XX 06-DEC-2000; 2000WO-US33029.  
 PF 06-DEC-1999; 99US-0169056.  
 XX 09-DEC-1999; 99US-0169866.  
 PR 09-DEC-1999; 99US-0169886.  
 PR 10-DEC-1999; 99US-0170252.  
 PR 12-JAN-2000; 2000US-0175740.  
 PR 05-DEC-2000; 2000US-0170252.  
 XX (CURA-) CURAGEN CORP.  
 XX Burgess CE, Prayaga SK, Shimkets RA, Rastelli L, Zerhusen BD;  
 PI Mezes PS;  
 DR WPI; 2001-374790/39.  
 DR N-PSDB; AAF83870.  
 XX Novel isolated human transmembrane, neuromedin peptide  
 PT gonadotropin-like protein and interleukin-1 receptor antagonist  
 PT proteins, useful for treating cancer, immune response disorder,  
 PT metabolic function disorders  
 XX  
 PS Claim 53; Fig 15B; 138pp; English.  
 XX The invention provides novel polypeptides (NOVX) selected from human  
 CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),  
 CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor  
 CC antagonist proteins (NOVINTRA A and B). The invention also provides  
 CC methods in which a NOVX polypeptide, polynucleotide and antibody are  
 CC used in the detection, prevention and treatment of a broad range of  
 CC pathological states. NOVTRAN can be used to treat a cell signaling  
 CC disorder such as cancer, immune response disorder, hematopoietic  
 CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat  
 CC endocrine disorder, muscle disorder, neurologic disorder, cancers of  
 CC central nervous system, breast, colon, ovary, kidney, prostate and  
 CC thyroid. NOVAGON can be used to treat reproductive development disorder,  
 CC metabolic function disorder and melanoma. NOVINTRA A and B can be used  
 CC to treat bone metabolism or structure disorder, inflammatory response  
 CC disorder, immune regulation disorder, septic shock, stroke, diabetes,  
 CC arthritis and cancer. The present sequence represents the NOVINTRA C  
 CC polypeptide.  
 XX  
 SQ Sequence 130 AA;  
 Query Match 77.8%; Score 646; DB 22; Length 130;  
 Best Local Similarity 95.5%; Pred. No. 3.6e-61;  
 Matches 126; Conservative 1; Mismatches 1; Indels 4; Gaps 2;  
 QY 17 DINHRVWVLDQTLIAVPRKDRMSPTIALISCRHVETLEKGRNPIYGLNGLNCLMC 76  
 DB 1 dinhrvwlqgdqtliaavprk--vfpvtialisrhrvhetlekdrngpiylglnlclmc 58  
 QY 77 AKVGDDPTLQLK--EKDINDLYNOPEPVKSFLEYHSQSGRNSTFESVAPGWFIVASSEG 134  
 DB 59 akvgddptlqlkqekdimdlynqpepvksflfhsqsgnrnstfesvafpgwfiavssg 118  
 QY 135 GCPLILTQELGK 146  
 DB 119 gcpliltqelgk 130  
 RESULT 5  
 ID AAW63136 standard; Protein; 169 AA.  
 XX  
 AC AAW63136;  
 XX  
 DT 14-OCT-1998 (first entry)  
 XX  
 DE Interleukin-1 receptor antagonist beta (IL-1ra-beta).  
 XX

KW Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;  
 KW IL-1 beta; inflammatory response; treatment; inflammation; septicaemia;  
 KW cancer; anaemia; arthritis; inflammatory bowel disease;  
 KW graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;  
 KW acute respiratory disease syndrome; psoriasis; restenosis;  
 KW traumatic brain injury; acquired immune deficiency syndrome;  
 KW cachexia.  
 XX Homo sapiens.  
 XX EP855404-A1.  
 XX 29-JUL-1998.  
 PD  
 XX 27-JAN-1998; 98EP-0300572.  
 XX 28-JAN-1997; 97US-0790032.  
 PR (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA  
 XX Young PR;  
 PI  
 XX WPI; 1998-389778/34.  
 DR N-PSDB; AAV42659.  
 XX  
 DR New nucleic acid encoding human interleukin-1 receptor antagonist  
 XX beta polypeptides - and related expression systems, transformed  
 PT cells, proteins, antibodies, agonists and antagonists, useful for  
 PT treatment, prevention and diagnosis of inflammation, septicaemia,  
 PT cancer etc  
 PT  
 PS Claim 13; Fig 2; 20pp; English.

XX The present sequence represents human Interleukin-1 receptor antagonist  
 CC beta (IL-1ra-beta). IL-1 alpha and IL-1 beta play key roles in  
 CC inflammatory responses, and are produced as zymogens which are cleaved  
 CC upon secretion to yield mature carboxyl terminal 17 kD fragments.  
 CC IL-1ra-beta polypeptides and polynucleotides are useful in treatment of  
 CC chronic and acute inflammation, septicaemia, cancer, anaemia, arthritis,  
 CC inflammatory bowel disease, graft vs. host rejection, autoimmunity,  
 CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),  
 CC psoriasis, restenosis, traumatic brain injury, acquired immune  
 CC deficiency syndrome (AIDS) and cachexia. These conditions (or  
 CC susceptibility to them) may be diagnosed by detecting mutations in the  
 CC IL-1ra-beta coding sequence analysing a sample for presence or amount  
 CC of IL-1ra-beta.  
 XX  
 XX Sequence 169 AA;

Query Match 56.2%; Score 466.5; DB 19; Length 169;  
 Best Local Similarity 59.9%; Pred. No. 7.4e-42;  
 Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;  
 QY 10 PQGSIQDINHVRVWLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYGLNG 69  
 DB 22 pitgtindlnqgwtlqggnlvavprsdsvtpvtvavtkcypealegrgdpilgln 81  
 QY 70 LNLCLMCAKVGDPQTLQLEKDIMLYNQPEPKVSKFLFVHSQSGRNSTFESVAFPGWFTA 129  
 DB 82 pemclycekvgeptqlqkeqkmdlygqpevpkpflyfraktgrtstlesvafpawfia 141  
 QY 130 VSSEGGCPILITQBLGKANTTDFGLTM 156  
 DB 142 -sskrdpiltselgksyntafeln 167

RESULT 6  
 ID AAY24043  
 XX AAY24043 standard; Protein; 169 AA.  
 AC AAY24043;  
 XX

DT 30-SEP-1999 (first entry)  
 XX A human SPOIL-I protein (also known as htANGO 080-I).  
 DE  
 XX SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;  
 KW bone metabolism disorder; proinflammatory disorder; immune disorder;  
 KW inflammatory disease; septic shock; stroke; diabetes; arthritis;  
 KW intercolitis; pneumonitis; epithelial cell; skin disease;  
 KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;  
 KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;  
 KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;  
 KW osteogenesis imperfecta; fibrous dysplasia; hypophosphatasia;  
 KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;  
 KW hypercalcaemia; bone mass; bone fragility; bone pain; bone deformity;  
 KW bone fracture; htANGO 80-I.  
 XX Homo sapiens.  
 OS  
 XX WO9937662-A1.  
 PN  
 XX 29-JUL-1999.  
 PD  
 XX 26-JAN-1999; 99WO-US01575.  
 PF  
 XX 27-JAN-1998; 98US-0013810.  
 PR  
 XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 PA  
 XX Busfield SJ;  
 XX WPI; 1999-458675/38.  
 DR N-PSDB; AAX86458.  
 DR  
 XX New isolated SPOIL proteins, used to develop products for treating,  
 PT e.g. inflammatory and immune disorders  
 PT  
 XX Example 1; Fig 4A-B; 126pp; English.

The present sequence represents a SPOIL-I protein. SPOIL proteins have  
 homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.  
 The SPOIL proteins are used as modulating agents in regulating a variety  
 of cellular processes. The products can be used for treating disorders  
 characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone  
 metabolism disorder, a proinflammatory disorder or an immune disorder.  
 They can be used for treating e.g. inflammatory diseases and disorders  
 e.g. inflammation, septic shock, stroke, diabetes, arthritis,  
 intercolitis and pneumonitis, epithelial cell and/or skin diseases and  
 disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma  
 and Kaposi's sarcoma and other epithelial cancers including squamous cell  
 carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and  
 bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's  
 disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,  
 fibrous dysplasia, hypophosphatasia, bone sarcoma, myeloma bone disorder  
 (e.g. osteolytic bone lesions) and hypercalcaemia. SPOIL molecules and  
 SPOIL modulators are useful for regulation of bone mass (e.g. increase in  
 bone mass and/or inhibit bone loss), management of bone fragility (e.g.  
 decrease bone fragility); and prevention and/or treatment of bone pain,  
 bone deformities and/or bone fractures. The products can also be used for  
 detection, diagnosis and screening assays.

XX Sequence 169 AA;  
 QY 10 PQGSIQDINHVRVWLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYGLNG 69  
 DB 22 pitgtindlnqgwtlqggnlvavprsdsvtpvtvavtkcypealegrgdpilgln 81  
 QY 70 LNLCLMCAKVGDPQTLQLEKDIMLYNQPEPKVSKFLFVHSQSGRNSTFESVAFPGWFTA 129  
 DB 82 pemclycekvgeptqlqkeqkmdlygqpevpkpflyfraktgrtstlesvafpawfia 141  
 QY 130 VSSEGGCPILITQBLGKANTTDFGLTM 156  
 DB 142 -sskrdpiltselgksyntafeln 167  
 Query Match 56.2%; Score 466.5; DB 20; Length 169;  
 Best Local Similarity 59.9%; Pred. No. 7.4e-42;  
 Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;

Db 82 pemclycekvgqptlqlkqekindlygqpevpkpflyraktgrtstlesvaifpdwfa 141  
 QY 130 VSSEGGCPILITQELGRANTDFGLTM 156  
 Db 142 -sskrdqpiiltselfgsyntafelni 167

RESULT 7  
 ID AAY24395  
 XX AAY24395 standard; Protein; 169 AA.  
 AC AAY24395;  
 XX  
 DT 20-SEP-1999 (first entry)  
 XX  
 DE Human interleukin-1 receptor antagonist beta.  
 XX  
 KW Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;  
 KW chronic inflammation; acute inflammation; arthritis; autoimmunity;  
 KW inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;  
 KW cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;  
 KW traumatic brain injury; AIDS; cachexia; allergy; parasite infection;  
 KW allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;  
 KW allergic inflammatory disease; delayed hypersensitivity; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9936541-A1.  
 XX  
 XX  
 PD 22-JUL-1999.  
 XX  
 PF 14-JAN-1999; 99WO-US00847.  
 XX  
 PR 29-APR-1998; 98US-0069619.  
 PR 14-JAN-1998; 98US-0007464.  
 XX  
 PA (SMTK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Marshall L, Young PR;  
 XX  
 DR WPI; 1999-430615/36.  
 DR N-PSDB; AAX90135.  
 XX  
 PT New interleukin-1 receptor antagonist beta, useful for treating  
 PT inflammation and autoimmune diseases  
 XX  
 PS Claim 15; Fig 1; 34pp; English.  
 XX  
 CC The present sequence represents human interleukin-1 receptor antagonist  
 CC beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are  
 CC useful for diagnosing diseases (or susceptibility to diseases) related  
 CC to the expression or activity of IL-1RA beta, by determining mutations  
 CC in the IL-1RA beta nucleic acid sequences and/or analysing for the  
 CC presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides  
 CC are also useful for screening for compounds which affect activity of the  
 CC protein. These can be used in treatment to inhibit (antagonist) or  
 CC enhance (agonist) IL-1RA beta activity, in addition to direct  
 CC administration of IL-1RA beta polypeptides to treat conditions, or  
 CC direct administration of antisense sequences to prevent expression.  
 CC IL-1RA beta polypeptides (administered directly, in a vector i.e. gene  
 CC therapy, and as a vaccine) and antibodies induce an immune response to  
 CC immunise and prevent disease. Diseases diagnosed, prevented or treated  
 CC include chronic and acute inflammation, septicemia, arthritis,  
 CC inflammatory bowel disease, graft vs. host disease, autoimmunity,  
 CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),  
 CC psoriasis, restenosis, traumatic brain injury, AIDS, cachexia, allergy,  
 CC parasite infection, allergic rhinitis, allergic asthma, atopic  
 CC dermatitis, allergic inflammatory diseases and delayed hypersensitivity.  
 XX  
 SQ Sequence 169 AA;

Query Match

56.2%; Score 466.5; DB 20; Length 169;

Best Local Similarity 59.9%; Pred. No. 7.4e-42;  
 Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;  
 QY 10 POQSGIODINHRVWVLODQTLIAVPRKDRMSPVTIALTSCRHVETLEKDCGNPIYLGLNG 69  
 Db 22 pitgtindngqwtlqggnlvavprdsdsvptvavltckypealeqgrdpilylgln 81  
 QY 70 LNLCLMACAKVGDPQPTQLKQEKDMDLYNQPEPVKSEFLYHSQSGRNSTFESVAPGWFIA 129  
 Db 82 pemclycekvgqptlqlkqekindlygqpevpkpflyraktgrtstlesvaifpdwfa 141  
 QY 130 VSSEGGCPILITQELGRANTDFGLTM 156  
 Db 142 -sskrdqpiiltselfgsyntafelni 167

## RESULT 8

AAE06656  
 ID AAE06656 standard; Protein; 169 AA.  
 XX  
 AC AAE06656;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Human interleukin-1epsilon (IL-1epsilon) protein.  
 XX  
 KW Human; interleukin-1epsilon; IL-1epsilon; virucide; hepatotropic; fever;  
 KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;  
 KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;  
 KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Binding-site 17..20 Location/Qualifiers  
 FT Binding-site 23 /note= "IL-1 receptor beta subunit binding region"  
 FT Region 23..27 /note= "IL-1 receptor beta subunit binding region"  
 FT Binding-site 28 /note= "Beta sheet region"  
 FT Binding-site 30..32 /note= "IL-1 receptor alpha subunit binding region"  
 FT Region 34..36 /note= "IL-1 receptor alpha subunit binding region"  
 FT Binding-site 36..38 /note= "Beta sheet region"  
 FT Region 42..45 /note= "IL-1 receptor alpha subunit binding region"  
 FT Binding-site 43 /note= "Beta sheet region"  
 FT Binding-site 45..50 /note= "IL-1 receptor alpha subunit binding region"  
 FT Binding-site 52 /note= "IL-1 receptor alpha subunit binding region"  
 FT Region 56..61 /note= "IL-1 receptor alpha subunit binding region"  
 FT Binding-site 61 /note= "Beta sheet region"  
 FT Binding-site 63 /note= "IL-1 receptor beta subunit binding region"  
 FT Binding-site 68 /note= "IL-1 receptor beta subunit binding region"  
 FT Binding-site 70..71 /note= "IL-1 receptor beta subunit binding region"  
 FT Binding-site 73 /note= "IL-1 receptor beta subunit binding region"  
 FT Binding-site 73..97 /note= "IL-1 receptor beta subunit binding region"  
 FT Region 74..79 /note= "IL-1 receptor alpha subunit binding region"  
 FT Region 84..89 /note= "Beta sheet region"



CC inflammatory conditions including arthritis, cholangitis, colitis,  
 CC encephalitis, endocarditis, glomerulonephritis, hepatitis, myocarditis,  
 CC pancreatitis, pericarditis, and reperfusion injury vasculitis. It is  
 CC also useful for treating immune-based diseases including conditions  
 CC involving T cells and/or macrophages e.g. acute and delayed  
 CC hypersensitivity, graft rejection, graft-versus-host disease;  
 CC autoimmune diseases including Type 1 diabetes mellitus and multiple  
 CC sclerosis. The composition may be used for treating bone and cartilage  
 CC resorption as well as diseases resulting in excess deposition of  
 CC extracellular matrix. Such diseases include osteoporosis, periodontal  
 CC diseases, interstitial pulmonary fibrosis, cirrhosis, systemic sclerosis  
 CC and keloid formation. It is also useful for treating tumours which  
 CC produce IL-1 as an autocrine growth factor and for preventing the  
 CC cachexia associated with certain tumours. It may be used for  
 CC treating neuronal diseases with an inflammatory component e.g.  
 CC Alzheimer's disease, stroke, depression and concussion injury and for  
 CC cardiovascular diseases in which recruitment of monocytes into the  
 CC subendothelial space plays a role, e.g. the development of  
 CC atherosclerotic plaques.  
 XX  
 SQ Sequence 169 AA;

Query Match 56.2%; Score 466.5; DB 22; Length 169;  
 Best Local Similarity 59.9%; Pred. NO. 7.4e-42;  
 Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;  
 QY 10 PQGGSTQDINHRVWLQDTLLAVPKDRMSPTTALISCRHVELEKDRGNPIVLGLNG 69  
 Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 22 pitgtlndlnqvwltlqgnlvavprsdsvtvtvavtckypealeqgrgdpilylqgn 81  
 QY 70 LNLCLMKAVGDOPTQLQLEKIDMDLYNOPEPVKSFVHVSQSGRNSFESVAFPGWFTA 129  
 Db ||| |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 82 pemclycekvgeoptqlkqekimldlygqpevpkpflyraktgrtstlesvafpdwfia 141  
 QY 130 VSSEGGCPILITQELGKANTDFGLTM 156  
 Db ||: |||:|||:|||:|||:  
 142 -sskrdqpiiltsekgkysntafelni 167

RESULT 10  
 AAU16937  
 ID AAU16937 standard; Protein; 173 AA.  
 XX  
 AC AAU16937;  
 XX  
 DT 07-NOV-2001 (first entry)  
 XX  
 DE Human novel secreted protein, SEQ ID 178.  
 XX  
 KW Human; immunosuppressive; antiarthritic; antirheumatic;  
 KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;  
 KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
 KW vulnary; secreted protein; rheumatoid arthritis;  
 KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
 KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;  
 KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
 KW corneal infection; wound healing; epithelial cell proliferation;  
 KW skin ageing; food additive; preservative; antiproliferative.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200155441-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 XX 17-JAN-2001; 2001WO-US01320.  
 PF 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-JUL-2000; 2000US-0218290.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR 26-JUL-2000; 2000US-0220964.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR 14-AUG-2000; 2000US-0225213.  
 PR 14-AUG-2000; 2000US-0225214.  
 PR 14-AUG-2000; 2000US-0225266.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 14-AUG-2000; 2000US-0225759.  
 PR 18-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226688.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227189.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0232400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235836.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.





XX Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;  
 KW inflammatory response; immune system; diagnosis; agonist; antagonist;  
 KW chemokine.  
 OS Mus sp.  
 XX WO9847921-A1.  
 XX 29-OCT-1998.  
 XX 17-APR-1998; 98WO-US06879.  
 XX 06-AUG-1997; 97US-0055111.  
 XX 21-APR-1997; 97US-0837627.  
 XX (SCHE ) SCHERING CORP.  
 XX Bazan JF, Hedrick JA, Kastelein RA, Sana TR;  
 PI WPI: 1998-609976/51.  
 DR N-PSDB; AAV71960.  
 XX Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.  
 PT regulating the immune system and inflammatory responses  
 XX Claim 1; Pages 92-93; 113pp; English.  
 XX This represents a rodent interleukin (IL)-1 epsilon polypeptide. The  
 CC invention relates to a recombinant polypeptide that specifically binds  
 CC polyclonal antibodies (Abs) generated against a 12 consecutive amino acid  
 CC segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these  
 CC IL polypeptides are used to regulate a cell involved in an inflammatory  
 CC response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are  
 CC used to produce Abs and antigen-Abs complexes. The polypeptides, Abs and  
 CC the corresponding nucleic acids regulate development and/or the immune  
 CC system, and can be used to diagnose and treat conditions associated with  
 CC abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1  
 CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,  
 CC IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1  
 CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion  
 CC protein with another cytokine or chemokine.  
 XX Sequence 160 AA;  
 SQ  
 Query Match 55.8%; Score 463; DB 19; Length 160;  
 Best Local Similarity 54.5%; Pred. No. 1.6e-41;  
 Matches 85; Conservative 30; Mismatches 41; Indels 0; Gaps 0;  
 QY 2 EKALKIDTPQOGSIQDINHRVWVLDQDTLIAVPRKDRMSPTVIALISCRHVETLEKDRGN 61  
 Db 4 ekeiraaasprlrvhqvdlssrvllqnliltavprkeqvtvltlpcqyldtletnrgd 63  
 QY 62 PYILGLNGLNLCMAKVGQDPTQLQKEKDMDLYNQPEPVKSFYHSGRNSTFESV 121  
 Db 64 ptymgvqrpmclctckdgcqvlqlgegnimemynkpevkasifhkhsgtstfesa 123  
 QY 122 APFGWFIASVSEGGCPILITQELGKANTTDFGLTML 157  
 Db 124 afggwfiavcskscpllttqelgeiftdfemiv 159  
 RESULT 14  
 ID AAY24049 standard; Protein; 160 AA.  
 XX AAY24049;  
 XX 30-SEP-1999 (first entry)  
 XX Amino acid sequence of a murine SPOIL-II protein.

KW SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;  
 KW bone metabolism disorder; proinflammatory disorder; immune disorder;  
 KW inflammatory disease; septic shock; stroke; diabetes; arthritis;  
 KW intercolitis; pneumonitis; epithelial cell; skin disease;  
 KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;  
 KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;  
 KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;  
 KW osteogenesis imperfecta; fibrous dysplasia; hypophosphatasia;  
 KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;  
 KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;  
 KW bone fracture.  
 XX Mus sp.  
 XX WO9937662-A1.  
 XX 29-JUL-1999.  
 XX 26-JAN-1999; 99WO-US01575.  
 XX 27-JAN-1998; 98US-0013810.  
 XX (MILL-) MILLENNIUM BIOTHEAPUEUTICS INC.  
 XX Busfield SJ;  
 XX WPI: 1999-458675/38.  
 XX N-PSDB; AAX86460.  
 XX New isolated SPOIL proteins, used to develop products for treating,  
 PT e.g. inflammatory and immune disorders  
 XX Claim 8; Fig 6; 126pp; English.  
 XX The present sequence represents a SPOIL-II protein. SPOIL proteins have  
 CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.  
 CC The SPOIL proteins are used as modulating agents in regulating a variety  
 CC of cellular processes. The products can be used for treating disorders  
 CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone  
 CC metabolism disorder, a proinflammatory disorder or an immune disorder.  
 CC They can be used for treating e.g. inflammatory diseases and disorders  
 CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,  
 CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and  
 CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma  
 CC and Kaposi's sarcoma and other epithelial cancers including squamous cell  
 CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and  
 CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's  
 CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,  
 CC fibrous dysplasia, hypophosphatasia, bone sarcoma, myeloma bone disorder  
 CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and  
 CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in  
 CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.  
 CC decrease bone fragility); and prevention and/or treatment of bone pain,  
 CC bone deformities and/or bone fractures. The products can also be used for  
 CC detection, diagnosis and screening assays.  
 XX Sequence 160 AA;  
 SQ  
 Query Match 55.8%; Score 463; DB 20; Length 160;  
 Best Local Similarity 54.5%; Pred. No. 1.6e-41;  
 Matches 85; Conservative 30; Mismatches 41; Indels 0; Gaps 0;  
 QY 2 EKALKIDTPQOGSIQDINHRVWVLDQDTLIAVPRKDRMSPTVIALISCRHVETLEKDRGN 61  
 Db 4 ekeiraaasprlrvhqvdlssrvllqnliltavprkeqvtvltlpcqyldtletnrgd 63  
 QY 62 PYILGLNGLNLCMAKVGQDPTQLQKEKDMDLYNQPEPVKSFYHSGRNSTFESV 121  
 Db 64 ptymgvqrpmclctckdgcqvlqlgegnimemynkpevkasifhkhsgtstfesa 123  
 QY 122 APFGWFIASVSEGGCPILITQELGKANTTDFGLTML 157  
 Db 124 afggwfiavcskscpllttqelgeiftdfemiv 159

Db 124 apgwfiaevskgscpliltqelgeiftdfemivv 159

RESULT 15  
AAU17010  
ID AAU17010 standard; Protein; 172 AA.  
XX  
AC AAU17010;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human novel secreted protein, SEQ ID 251.  
XX  
KW Human; immunosuppressive; antiarthritic; antirheumatic;  
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;  
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
KW vulnary; secreted protein; rheumatoid arthritis;  
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
KW corneal infection; wound healing; epithelial cell proliferation;  
KW skin ageing; food additive; preservative; antiproliferative.  
XX  
OS Homo sapiens.  
XX  
XX WO200155441-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01320.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-MAR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 23-AUG-2000; 2000US-0227182.  
PR 30-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 05-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
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PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 01-NOV-2000; 2000US-0241826.  
PR 08-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0244674.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246529.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.







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OM protein - protein search, using sw model

Run On: June 20, 2002, 15:03:51 ; Search time 36.86 Seconds  
(without alignments)  
411.886 Million cell updates/sec

Title: US-09-763-498-8  
Perfect score: 830  
Sequence: 1 MEKALKIDTPQQGSIQDINH.....ILTQELGKANTTDFGLTMLF 158

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR-71:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195.5	23.6	178	2 A44610	interleukin-1 rece
2	190.5	23.0	178	2 C40956	interleukin-1 rece
3	185.5	22.3	155	2 JC7104	interleukin-1 rece
4	183.5	22.1	177	2 A30368	interleukin-1 rece
5	183.5	22.1	180	2 A39386	interleukin-1 rece
6	173.5	20.9	266	1 S23010	interleukin-1 beta
7	170.5	20.5	177	2 A54377	interleukin-1 rece
8	170	20.5	266	1 ICBO1B	interleukin-1 beta
9	160	19.3	267	2 S38373	interleukin-1 beta
10	155	18.7	267	1 JN0724	interleukin-1 beta
11	143.5	17.3	269	1 ICH01B	interleukin-1 beta
12	141.5	17.0	268	1 A30594	interleukin-1 beta
13	138.5	16.7	214	2 JC5646	interleukin-1 beta
14	121	14.6	269	1 I55969	interleukin-1 beta
15	81	9.8	256	2 F86463	hypothetical prote
16	79	9.5	501	2 AG0939	glycerol kinase [i
17	77	9.3	268	1 ICBO1A	interleukin-1 alph
18	77	9.3	268	1 A61246	interleukin-1 alph
19	77	9.3	502	1 K1ECCL	glycerol kinase (E
20	77	9.3	502	2 C91235	glycerol kinase [i
21	77	9.3	509	2 C86082	glycerol kinase [i
22	75.5	9.1	270	1 S10532	interleukin-1 alph
23	75	9.0	15281	2 S41309	cyclosporin synthe
24	74.5	9.0	1077	2 T01474	hypothetical prote
25	74	8.9	407	2 T22554	hypothetical prote
26	73.5	8.9	1320	2 H64090	phosphoribosylform
27	73	8.8	403	2 AC2271	precorrin-6y-depen
28	73	8.8	837	2 T48407	hypothetical prote
29	72.5	8.7	325	2 E87125	ribonucleotide red

## ALIGNMENTS

RESULT 1

A44610  
interleukin-1 receptor antagonist precursor - mouse  
N;Alternate names: IL-1Ra  
C;Species: Mus musculus (house mouse)  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 16-Jul-1999  
C;Accession: A44610; B40956; A49031; I56106; I52970  
R;Matsushima, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.  
Blood 78, 616-623, 1991  
A;Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrop  
A;Reference number: A44610; MUID:91316273  
A;Accession: A44610  
A;Molecule type: mRNA  
A;Residues: 1-178 <MAT>  
A;Cross-references: GB:M64404; NID:q198296; PIDN:AAA39277.1; PID:q198297  
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thoms  
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991  
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fami  
A;Reference number: A40956; MUID:91271363  
A;Accession: B40956  
A;Molecule type: DNA  
A;Residues: 7-178 <EIS>  
A;Cross-references: GB:M63100; NID:q198389; PIDN:AAA39310.1; PID:q198390  
R;Shuck, M.E.; Bessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.  
Eur. J. Immunol. 21, 2775-2780, 1991  
A;Title: Cloning, heterologous expression and characterization of murine interleukin  
A;Reference number: A49031; MUID:92037824  
A;Accession: A49031  
A;Molecule type: mRNA  
A;Residues: 23-178 <SHU>  
A;Cross-references: GB:S64082; NID:q238584; PIDN:AAB20265.1; PID:q238585  
A;Experimental source: peritoneal macrophages, ICR strain  
A;Note: sequence extracted from NCBI backbone (NCBIN:64082, NCBI:64085)  
R;Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.  
J. Immunol. 146, 4228-4233, 1991  
A;Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene map  
A;Reference number: I56106; MUID:91250712  
A;Accession: I56106  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-178 <RES>  
A;Cross-references: GB:M74294; NID:q198387; PIDN:AAA39309.1; PID:q198388  
R;Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.  
Cytokine 6, 1-9, 1994  
A;Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regu  
A;Reference number: I52970; MUID:94271931  
A;Accession: I52970  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-178 <RE2>  
A;Cross-references: GB:I32838; NID:q487864; PIDN:AAA20576.1; PID:q528978  
C;Genetics:

chitin deacetylase  
translation initia  
3-dehydroquinat d  
hypothetical prote  
homeotic protein C  
interleukin-1 alph  
interleukin-1 alph  
B-cell antigen CD1  
translation initia  
valine--tRNA ligas  
siderophore/surfac  
probable MAP kinas  
interleukin-1 alph  
conserved hypoteth  
ornithine carbamoy  
proteinase [import  
proteinase IV, pro

30 72.5 8.7 421 2 A47713  
31 72 8.7 1132 2 T43483  
32 71.5 8.6 325 2 S48698  
33 71.5 8.6 460 2 AG2262  
34 71 8.6 1426 2 T30817  
35 70.5 8.5 270 2 I46620  
36 70.5 8.5 556 2 A44441  
37 70.5 8.5 944 2 G86720  
38 70.5 8.5 1093 2 T51503  
39 70 8.4 447 2 H97146  
40 70 8.4 516 2 H84424  
41 69.5 8.4 268 1 B24073  
42 69.5 8.4 454 2 G70476  
43 69 8.3 327 1 OWPSY  
44 69 8.3 333 2 B86567  
45 69 8.3 333 2 G72058



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QY 15 IODINHRVWVLDQDTLTA-----VPRKDMSPVTIALISCRHVTLEKDRGNPTIYGL 67
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Db 43 IWDVNOKTFYJURNQLVAGYVGGPNVLEBKIDVVP-----EPHALFLGI 88
      | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 68 NGLNLCLCMKAVGDPQPTLOLKEKDIMLYNQPEPKVSFLFYHSQSGRNSTFESVAPPGWF 127
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 89 HGGKMLCSVCKSGDGETRLOLEAVNITDLSNRKQDKRFKFAIRSDSGPTTSFESACPGWF 148
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QY 128 IAVSEGGCPILILTOELGKANTTDFGL 154
      : : : : | : | : | : | : | : | : | : | : | : | : |
Db 149 LCTAMEADQPVSLT-----NMPDEGV 169
      : : : : | : | : | : | : | : | : | : | : | : | : |

RESULT 6
S23010
interleukin-1 beta precursor - sheep
N:Alternate names: hematopoietin-1; IL-1 beta
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999
C:Accession: S23010; S43047; S13092; B61246
R:Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A:Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
A:Reference number: S23010; MUID:92119335
A:Accession: S23010
A:Molecule type: mRNA
A:Residues: 1-266 <SEO>
A:Cross-references: EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809
A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in
R:Sargan, D.R.
submitted to the EMBL Data Library, May 1992

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A:Molecule type: mRNA  
A:Residues: 1-13,'C','L',15-54,'K','S',63,'A','G',65-144,'L',146-266 <SAR>  
A:Cross-references: EMBL:X54796; NID:g1273; PIDN:CA38566.1; PID:g1274  
R:Fiskerstrand, C.; Sargan, D.  
Nucleic Acids Res. 18, 7165, 1990  
A:title: Nucleotide sequence of ovine interleukin-1 beta.  
A:Reference number: S13092; MUID:91088326  
A:Accession: S13092  
A:Molecule type: mRNA  
A:Residues: 1-13,'C','L',15-54,'K','S',63,'A','G',65-144,'L',146-266 <FIS>  
A:Cross-references: EMBL:X54796  
A>Note: the authors translated the codon AGT for residue 62 as Arg  
R:Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.  
Immunology 74, 453-460, 1991  
A:title: Molecular cloning and characterization of ovine IL-1alpha and IL-1-beta.  
A:Reference number: A61246; MUID:92120716  
A:Accession: B61246  
A:Molecule type: mRNA  
A:Residues: 1-144,'L',146-266 <AND>  
C:Comment: This protein lacks a conventional signal sequence for protein ex-  
ved form of interleukin-beta, unlike interleukin 1-alpha, is inactive.  
C:Comment: Interleukin-lbeta precursor is less heavily myristoylated than i  
C:Genetics:  
A:Gene: IL-1-beta  
C:Superfamily: interleukin-1  
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophag  
E:114-266/Product: Interleukin-1 beta #status predicted <WAT>

Query Match            20.9%; Score 173.5; DB 1; Length 266;  
Best Local Similarity    30.8%; Pred. No. 1.2e-09;  
Matches 48; Conservative 27; Mismatches 62; Indels 19; Gaps

QY         2 EKALKDTFQQSGIQDINRWVLOQTLLIAPVRKDRMSPTYIALISRHHVETLEKGRGN 61  
            : : | : | : |  
Db       128 QKSVLVDSP-----CVLK---ALHLPQSQRMSRVFFVCN---SFVQGERDNKI 169  
            : : | : | : |  
QY       62 PIYLGLNGLNLCIMCAKVGDQPTFLQLKEKDINDLYNQPEPKVSFLFYHSQSRNSTFSV 121  
            : : | : | : |

Db 170 PVALGIRDKNLVSLCKVKGDTPTLQLEEDV-PKVYPKRNMEKRFVYFKTEIKNTVEFESV 228

QY 122 APFGWFIASVSEGGCPILITQELGKANTTDFGLTML 157

Db 229 LYPNWIYSTQIEBKPVFLGRFGGQDITDFRMETL 264

## RESULT 7

AS4377

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Jul-1999

C:Accession: A54377; 146729

R:Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M.T.

J. Biol. Chem. 269, 6962-6971, 1994

A:Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional chara

A:Reference number: A54377; MUID:94165101

A:Accession: A54377

A:Molecule type: mRNA

A:Residues: 1-177 <COM>

A:Cross-references: GB:S68977; NID:9545740; PIDN:AAB30093.1; PID:9545741

A:Experimental source: colon tissue

A:Note: sequence extracted from NCBI backbone (NCBIN:144168, NCBIP:144169)

R:Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.; Mori, S.; Furukawa, S.; Maeda

Immunology 77, 235-244, 1992

A:Title: Interleukin-1 receptor antagonist in inflammatory exudate cells of rabbits. Prod

A:Reference number: 146729; MUID:93052512

A:Accession: 146729

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-177 <GOT>

A:Cross-references: GB:D21832; NID:9425787; PIDN:BAA04860.1; PID:9452205

C:Superfamily: Interleukin-1

C:Keywords: cytokine receptor; extracellular protein; glycoprotein

F:1-25/Domain: signal sequence #status predicted <SIG>

F:109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.5%; Score 170.5; DB 2; Length 177;

Best Local Similarity 30.6%; Pred. No. 1.5e-09;

Matches 44; Conservative 21; Mismatches 52; Indels 27; Gaps 3;

QY 15 IQDINHRVWVLDQDTLFA-----VPRKDRMSPTVIALISCRHVETLEKDRGNPIYLGL 67

Db 40 IWDVYQKTFYLRNNQVAGVLOGPNKLEERIDVPL-----EPQLLEFLGI 85

QY 68 NGLNLCIMCAKVGDPDTLQLEKDIMDLNQPEPVKSFLEYHSQSGRNSTFESVAPFGWF 127

Db 86 QRKGLCLSLCKVSGDKMKHLHLEAVNITDGNKQDQKRFTRFIRNSGPTTTFESASCPGWF 145

QY 128 IAVSSEGGCPILITQELGKANTTD 151

Db 146 LCTALEADQPVSLT-----NTPD 163

## RESULT 8

ICB01B

Interleukin-1 beta precursor - bovine

N:Alternate names: hematopoietin-1; IL-1 beta

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 22-Jun-1999

C:Accession: J00010; S01380

R:Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.

Mol. Immunol. 25, 429-437, 1988

A:Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin

A:Reference number: A94695; MUID:88318652

A:Accession: J00010

A:Molecule type: mRNA

A:Residues: 1-266 <MAL>

A:Cross-references: GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201

R:Leong, S.R.; Flaggs, G.M.; Lawman, M.; Gray, P.W.

Nucleic Acids Res. 16, 9054, 1988

A:Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.

A:Reference number: S01380; MUID:89016591

A:Accession: S01380

A:Molecule type: mRNA

A:Residues: 1-251, 'A', 253-266 <LEO>

A:Cross-references: EMBL:X12498; NID:9448; PIDN:CAA31018.1; PID:94449

C:Comment: This protein is a cytokine that mediates a variety of immunoregulatory and  
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.

C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin

C:Superfamily: interleukin-1

C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen

F:114-266/Product: interleukin-1 beta #status predicted <MA>

Query Match 20.5%; Score 170; DB 1; Length 266;

Best Local Similarity 31.6%; Pred. No. 2.7e-09;

Matches 49; Conservative 23; Mismatches 75; Indels 8; Gaps 4;

QY 8 DTPOQG---SIQDINHRVWVLDQDTLIAVPR--KDRMSPTVIALISCRHVETLEKDRGNP 62

Db 113 DAPVQSIKCKLDREKQSLVLAAPCVLKALHLSQEMNRVVFVCM--FVQGEERDNKIP 170

QY 63 IYLGNGNLCLIMCAKVGDPDTLQLEKDIMDLNQPEPVKSFLEYHSQSGRNSTFESVA 122

Db 171 VALGIKDKNLVSLSCVKKGDTPTLQLEEDV-PKVTPKRNMEARFVYFKTEIKNTVEFESVL 229

QY 123 PFGWFIASVSEGGCPILITQELGKANTTDFGLTML 157

Db 230 YPNWYISTQIEERPVFLGHFRGGQDITDFRMETL 264

## RESULT 9

S38373

Interleukin-1 beta precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 20-May-1994 #sequence\_revision 01-Dec-1995 #text\_change 16-Jul-1999

C:Accession: S38373

R:Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; O

Eur. J. Biochem. 217, 45-52, 1993

A:Title: Gene sequence, cDNA construction, expression in Escherichia coli and genetic

A:Reference number: S38373; MUID:94039070

A:Accession: S38373

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-267 <VAN>

A:Cross-references: EMBL:X74568; NID:9407899; PIDN:CAA52660.1; PID:9407900

C:Genetics:

A:Insertions: 16/2; 33/3; 99/1; 154/1; 197/3

C:Superfamily: interleukin-1

Query Match 19.3%; Score 160; DB 2; Length 267;

Best Local Similarity 29.0%; Pred. No. 2.7e-08;

Matches 45; Conservative 27; Mismatches 73; Indels 10; Gaps 4;

QY 9 TPOQG---SIQDINHRVWVLDQDTLIAVPRKDRMSPTVIALISCRHVETLEKDRGNP 62

Db 115 TPVQSVDCDKLDKDEKALVLAGPHELKALHLLKGLDKREWFECM---SFVQGDSDDKIP 171

QY 63 IYLGNGNLCLIMCAKVGDPDTLQLEKDIMDLNQPEPVKSFLEYHSQSGRNSTFESVA 122

Db 172 VYLGKGNLVLSCVMKDDPTPLQLEDVDPKS-YPKRDMKREVFYFKTEIKNRVFESAL 230

QY 123 PFGWFIASVSEGGCPILITQELGKANTTDFGLTML 157

Db 231 YPNWYISTQAEQKPVFLGNLKGRODITDFTMEVL 265

## RESULT 10

JN0724

Interleukin-1 beta precursor - pig

N:Alternate names: hematopoietin-1; IL-1 beta

C:Species: Sus scrofa domestica (domestic pig)

A:Cross-references: GB:K02770; NID:g1862268; PIDN:AAA36106.1.; PID:g307043  
R:March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, J.  
Nature 315, 641-647, 1985  
A:Title: Cloning, sequence and expression of two distinct human interleukin-1 components  
A:Reference number: A93361; MUID:85240547  
A:Accession: A93361  
A:Molecule type: mRNA  
A:Residues: 1-269 <MAR>  
A:Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1.; PID:g33790  
A:Note: parts of this sequence, including the amino end of the mature form, were confirmed by  
R:Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolffe, S.M.;  
Adv. Gene Technol. 22, 339-340, 1985  
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.  
A:Reference number: I51852  
A:Accession: I51852  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-5, 'K', 'I', '19, 'H', '21-110, 'Q', '112-176, 'A', '178-213, 'P', '215-269 <WEB>  
A:Cross-references: GB:M54933; NID:g186287; PIDN:AAA59136.1.; PID:g186288  
R:Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; H  
Biochem. Biophys. Res. Commun. 143, 345-352, 1987  
A:Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.  
A:Reference number: I52217; MUID:87156769  
A:Accession: I65200  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-269 <NLTS>  
A:Cross-references: GB:ML5330; NID:g186283; PIDN:AAA59135.1.; PID:g307045  
R:Kotenko, S.V.; Bulecnok, M.T.; Veilko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov  
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989  
A:Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin-1  
A:Reference number: I38131; MUID:90249285  
A:Accession: I38132  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-269 <KOT>  
A:Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1.; PID:g35663  
R:Zsebo, K.M.; Wypych, J.; Yuschenko, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, Y.  
Blood 71, 962-968, 1988  
A:Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic  
A:Reference number: A90732; MUID:88184226  
A:Accession: B27616  
A:Molecule type: protein  
A:Residues: 117-123, 'X', '125-126, 'X', '128 <ZSE>  
R:Stevenson, F.T.; Burstein, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.  
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993  
A:Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysine  
A:Reference number: A48293; MUID:93348250  
A:Contents: annotation; myristylation of lysines  
R:Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.  
Biochim. Biophys. Acta 1118, 25-35, 1991  
A:Title: The role of arginine residues in interleukin 1 receptor binding.  
A:Reference number: S19608; MUID:92110334  
A:Contents: annotation; type 1 IL-1 receptor interaction site  
A:Note: modification of Arg-120 by phenylglyoxal blocks receptor binding  
R:Clow, G.M.; Gronenborn, A.M.  
submitted to the Brookhaven Protein Data Bank, January 1991  
A:Reference number: A50049; PDB:6T1B  
A:Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269  
R:Clow, G.M.; Wingfield, P.T.; Gronenborn, A.M.  
Biochemistry 30, 2315-2323, 1991  
A:Title: High-resolution three-dimensional structure of interleukin 1beta in solution  
A:Reference number: A44675; MUID:91159409  
A:Contents: annotation; (1)H-NMR structural determination  
R:Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.  
J. Biol. Chem. 266, 7081-7086, 1991  
A:Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a  
A:Reference number: A39774; MUID:91201363  
A:Contents: annotation  
R:Finzel, B.C.; Watenpugh, K.D.; Einspahr, H.M.  
submitted to the Brookhaven Protein Data Bank, December 1989  
A:Reference number: A50016; PDB:1T1B



Search completed: June 20, 2002, 15:03:52  
Job time: 162 sec

Query Match		9.8%; Score 81; DB 2;	Length 256;
Best Local Similarity		25.2%; Pred. No. 1.8;	
Matches 32; Conservative 10; Mismatches 45; Indels 32; Gaps 6;			
QY	30	LIAVPRKORMSVTTALISCRHVTELEKDRCGNPTIYLGLNCLNLCAKVGPDIQLKE	89
	:::	: : :::::	:
Dd	22	MVASLEESGSLPVTVDLLTGC-----GFNM----	TDTNTVSTLEEYS 58
	:	:	:
QY	90	KIMIDILYNQPEPVKSFTLYHSQSGRNSTFESVAFP-----GWFIAYS--SEGCGPL-IL	140
	:	: :	:
Dd	59	KPLIDLLENLPPEEKVILVGHTGGASISIALERFFPEKISKATFCVCAWVSQGQRPFDFV	118
	:	:	:
QY	141	TOELCKA	147
	:	:	:
Dd	119	SBEELGSA	125



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OM protein - protein search, using sw model

Run on: June 20, 2002, 15:11:19 ; Search time 19.43 Seconds  
(without alignments)  
314.858 Million cell updates/sec

Title: US-09-763-498-8  
Perfect score: 830  
Sequence: 1 MEKALKIDTPQGSIQDINH.....ILTQELGKANTIDGLTLMF 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	195.5	23.6	1 IL1X_MOUSE	P25085 mus musculus
2	190.5	23.0	1 IL1X_RAT	P25086 rattus norv
3	186.5	22.5	1 IL1X_HORSE	O18999 equus caball
4	183.5	22.1	1 IL1X_HUMAN	P18510 homo sapien
5	178.5	21.5	1 IL1X_PIG	Q29056 sus scrofa
6	173.5	20.9	1 IL1B_SHEEP	P21621 ovis aries
7	172.5	20.8	1 IL1X_BOVIN	O77482 bos taurus
8	170.5	20.5	1 IL1X_RABBIT	P26890 oryctolagus
9	167	20.1	1 IL1B_CEREL	P51745 cervus elap
10	164	19.8	1 IL1B_BOVIN	P09428 bos taurus
11	162.5	19.6	1 IL1B_CAPHI	P79162 capra hircu
12	155	18.7	1 IL1B_PIG	P26889 sus scrofa
13	145.5	17.5	1 IL1B_MACFA	P79182 macaca fasc
14	145.5	17.5	1 IL1B_MACFA	P48090 macaca mula
15	143.5	17.3	1 IL1B_HUMAN	P01584 homo sapien
16	143.5	17.3	1 IL1B_MACNE	P15493 macaca neme
17	142.5	17.2	1 IL1B_CAVPO	Q9wvg1 cavia porce
18	141.5	17.0	1 IL1B_RABIT	P4628 oryctolagus
19	137.5	16.6	1 IL1B_CERTO	P46648 cercopithec
20	133.5	16.1	1 IL1B_HORSE	Q28386 equus caball
21	128	15.4	1 IL1B_HORSE	Q63264 rattus norv
22	127.5	15.4	1 IL1B_FELCA	P41687 felis silve
23	121	14.6	1 IL1B_MOUSE	P10749 mus musculus
24	120.5	14.5	1 IL1B_TRIVU	Q9xs77 trichosurus
25	82	9.9	1 IL1A_HORSE	Q28385 equus caball
26	79	9.5	1 IL1A_CAPHI	P79161 capra hircu
27	79	9.5	1 IL1A_FELCA	O46613 felis silve
28	77	9.3	1 IL1A_BOVIN	P08831 bos taurus
29	77	9.3	1 GLPK_ECOLI	P08859 escherichia
30	75.5	9.1	1 IL1A_PIG	P18430 sus scrofa
31	75	9.0	1 CUT2_HUMAN	O14529 homo sapien
32	74	8.9	1 IL1A_SHEEP	Q28579 ovis aries
33	73.5	8.9	1 PUR4_HAEIN	P43847 haemophilus

34	72.5	8.7	325	1	RIR2_MYCLE	Q9cbq2 mycobacteri
35	72.5	8.7	421	1	CHDE_MUCRO	P50325 mucor rouxi
36	72.5	8.7	950	1	IF2_LACLC	Q9x764 lactococcus
37	72	8.7	1220	1	IF2P_HUMAN	O60841 homo sapien
38	72	8.7	1955	1	PC15_HUMAN	Q96qu1 homo sapien
39	71.5	8.6	194	1	IL18_RAT	P97636 rattus norv
40	71	8.6	872	1	MGR2_HUMAN	Q14416 homo sapien
41	71	8.6	1426	1	CUT2_MOUSE	P70298 mus musculu
42	71	8.6	1943	1	PC15_MOUSE	Q99pj1 mus musculu
43	70.5	8.5	271	1	IL1A_MACFA	P79340 macaca fasc
44	70.5	8.5	556	1	CD19_HUMAN	P15391 homo sapien
45	70.5	8.5	944	1	IF2_LACLA	P58002 lactococcus

## ALIGNMENTS

RESULT	1
IL1X_MOUSE	
ID	IL1X_MOUSE
AC	P25085; O70207;
DT	01-MAY-1992 (Rel. 22, Created)
DT	01-MAY-1992 (Rel. 22, Last sequence update)
DE	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE	(IRAP).
GN	IL1RN OR IL-1RA.
OS	Mus musculus (Mouse).
OC	Eumariota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RN	SEQUENCE FROM N.A. (ISOFORM 1).
RX	MEDLINE=91250712; PubMed=1828262;
RA	Zahedi K., Seldin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;
RT	"Mouse IL-1 receptor antagonist protein. Molecular characterization,
RT	gene mapping, and expression of mRNA in vitro and in vivo.";
RL	J. Immunol. 146:4228-4233(1991).
RN	[2]
RN	SEQUENCE FROM N.A. (ISOFORM 1).
RX	MEDLINE=91316273; PubMed=1830498;
RA	Matsushima H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J.;
RT	"Cloning and expression of murine interleukin-1 receptor antagonist
RT	in macrophages stimulated by colony-stimulating factor 1.";
RL	Blood 78:616-623(1991).
RN	[3]
RN	SEQUENCE FROM N.A. (ISOFORM 1).
RP	STRAIN=SWISS;
RC	MEDLINE=94271931; PubMed=8003626;
RX	Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;
RA	"The mouse interleukin 1 receptor antagonist protein: gene structure
RT	and regulation in vitro.";
RL	Cytokine 6:1-9(1994).
RN	[4]
RN	SEQUENCE FROM N.A. (ISOFORM 2).
RP	STRAIN=FVBXDBA/1 LACJ;
RC	MEDLINE=98209757; PubMed=9550387;
RX	Gabay C., Porter B., Fantuzzi G., Arend W.P.;
RA	"Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning
RT	and protein expression of intracellular isoform and tissue
RT	distribution of secreted and intracellular IL-1 receptor antagonist in
RT	vivo.";
RL	J. Immunol. 159:5905-5913(1997).
RN	[5]
RN	SEQUENCE OF 7-178 FROM N.A.
RP	MEDLINE=91271363; PubMed=1828896;
RX	Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA	Brandhuber B.J., Thompson R.C.;
RT	"Interleukin 1 receptor antagonist is a member of the interleukin 1
RT	gene family: evolution of a cytokine control mechanism.";
RL	Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN	[6]
RN	SEQUENCE OF 23-178 FROM N.A.

```

RX MEDLINE-92037824; PubMed-1834470;
RA Shuck M.E., Eessalu T.E., Tracey D.E., Bienkowski M.J.;
RT "Cloning, heterologous expression and characterization of murine
RT Interleukin 1 receptor antagonist protein.";
RL Eur. J. Immunol. 21:2775-2780(1991).
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -!- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR
CC (ISOFORM 2).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M74294; AAA39309.1; -
DR EMBL; M64404; AAA39277.1; -
DR EMBL; L32838; AAA20576.1; -
DR EMBL; AF001795; AAC15251.1; -
DR EMBL; M57525; AAA39278.1; -
DR EMBL; M63100; AAA39310.1; -
DR EMBL; S64082; AAB20265.1; -
DR PIR; B40956; B40956.
DR PIR; A44610; A44610.
DR HSSP; P18510; IL1R.
DR MGD; MGI:96547; Il1rn.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 92 142 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 1 21 MEICGYPYSLISLLILFH -> MA (IN ISOFORM
FT SEQUENCE 178 AA; 20274 MW; 84AA002A3119C024 CRC64;
Query Match 23.6%; Score 195.5; DB 1; Length 178;
Best Local Similarity 35.1%; Pred. No. 2.8e-13;
Matches 47; Conservative 21; Mismatches 45; Indels 21; Gaps 2;
QY 15 IQDINHRVWVLQDQTLLIA-----VPRKDRMSPTVIALISCRHVTLEKDRGNPIYLGL 67
DB 41 IWDTNQKTFYLRNQLIAGYLGQPNTKLEEKIDMVPIDFRNV-----VFLGI 86
QY 68 NGLNLCIMKAVGDPDTLOLKEKDMDLYNQPEPKVKSFLFVHSQSGRNSFTFESVAPFGWF 127
DB 87 HGGKLCISCAKSGDDIKLQLEEVNITDLNKNKEEDKRFTFIRSEKPTTSFESAACPGWF 146
QY 128 IAVSSEGGCPILIT 141
DB 147 LCTTLEADRPVSLT 160
RESULT 2
IL1X_RAT STANDARD; PRT; 178 AA.
AC P25086;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
(ILRAP).
GN IL1RN OR IL-1RA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91271363; PubMed-1828896;
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandhuber B.J., Thompson R.C.;
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT gene family: evolution of a cytokine control mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; M63101; AAA41434.1; -
DR PIR; C40956; C40956.
DR HSSP; P18510; IL1R.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 92 142 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 178 AA; 20282 MW; F3A5754FB6C51B03 CRC64;
Query Match 23.0%; Score 190.5; DB 1; Length 178;
Best Local Similarity 35.1%; Pred. No. 9.3e-13;
Matches 46; Conservative 20; Mismatches 50; Indels 15; Gaps 2;
QY 15 IQDINHRVWVLQDQTLLIA-----VPRKDRMSPTVIALISCRHVTLEKDRGNPIYLGL 70
DB 41 IWDTNQKTFYLRNQLIAGYLGQPNTKLEEKIDMVPIDFRNV-----FLGIHG 89
QY 71 NLCLMCAKVGDPDTLOLKEKDMDLYNQPEPKVKSFLFVHSQSGRNSFTFESVAPFGWFI 130
DB 90 KLCISCAKSGDDIKLQLEEVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFI 149
QY 131 SSEGCPILIT 141
DB 150 TLEADHPVSLT 160
RESULT 3
IL1X_HORSE STANDARD; PRT; 177 AA.
AC O18999; 077745;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL1RA.
OS Equus caballus (Horse).

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DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)  
 DE (IRAP).  
 GN IL1RN OR IRAP1.  
 OS Sus scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CROSSBREED; TISSUE=Lung;  
 RA Yin J., Murtaugh M.P.;  
 RT "Characterization of IRAP in morphine treated pig."  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS  
 CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 CC  
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 CC  
 CC EMBL; L38849; AAA99424.1; -.  
 DR HSSP; P18510; IIRA.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 DR PRINTS; PR00264; INTERLEUKIN1.  
 DR ProDom; PD002536; Interleukin\_1; 1.  
 DR SMART; SM00125; IL1; 1.  
 DR SMART; PS00253; INTERLEUKIN\_1; 1.  
 DR Glycoprotein; Signal.  
 KW SIGNAL 1 25 BY SIMILARITY.  
 FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST  
 FT PROTEIN.  
 FT DISULFID 91 141 BY SIMILARITY.  
 FT CARBOHYD 109 109 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 177 AA; 20093 MW; 2114DC6119A9D5F9 CRC64;  
  
 Query Match 21.5%; Score 178.5; DB 1; Length 177;  
 Best Local Similarity 32.4%; Pred. No. 1.6e-11;  
 Matches 44; Conservative 20; Mismatches 47; Indels 25; Gaps 2;  
  
 QY 15 IQDINHRVWVLODQTLLA-----VPRKDEMSPTIALISCRHVTLEKDRGNPIYL 65  
 DB 40 IWDVYQTFYLRNQLVAGYLOQNTKLEKIDVFPV-----EPHFVFL 83  
  
 QY 66 GLGLNGLCLMCAKVGDOPTLQLEKIDIMLYNOPEPVKSFLEYHSQSGRNSTFESVAFPG 125  
 DB 84 GIHGKGLCLSCVSGDEMKQLQDAVNITDLRNSEQDKRFTFIRSDSGPTTSFESAACPG 143  
  
 QY 126 WFIASVSEGGCPILLT 141  
 DB 144 WFLTALEADQPVGLT 159  
  
 RESULT 6  
 IL1B\_SHEEP  
 ID IL1B\_SHEEP STANDARD; PRT; 266 AA.  
 AC P21621;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 30-MAR-2000 (Rel. 39, Last annotation update)  
 DE Interleukin-1 beta precursor (IL-1 beta).  
 GN IL1B.  
 OS Ovis aries (Sheep).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Caprinae; Ovis.

OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92119335; PubMed=1840515;  
 RA Seow H.F., Rothel J.S., David M.J., Wood P.R.;  
 RT "Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.";  
 RL DNA Seq. 1:423-426(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91088326; PubMed=2263490;  
 RA Fiskerstrand C., Sargan D.;  
 RT "Nucleotide sequence of ovine interleukin-1 beta.";  
 RL Nucleic Acids Res. 18:7165-7165(1990).  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS  
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
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 CC  
 CC EMBL; X54796; CAA38566.1; -.  
 DR EMBL; X56972; CAA40293.1; -.  
 DR PIR; S13092; S13092.  
 DR PIR; S13810; S13810.  
 DR PIR; S23010; S23010.  
 DR HSSP; P01584; S1IB.  
 DR InterPro; IPR002348; IL1\_HBGF.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR InterPro; IPR003502; Interleukin\_1\_prop.  
 DR Pfam; PF00340; IL1; 1.  
 DR Pfam; PF02394; IL1\_propep; 1.  
 DR PRINTS; PR00262; IL1HBGF.  
 DR ProDom; PD002536; Interleukin\_1; 1.  
 DR SMART; SM00125; IL1; 1.  
 DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
 KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.  
 FT PROPEP 1 113  
 FT CHAIN 114 266 INTERLEUKIN-1 BETA.  
 FT CONFLICT 14 14 Y -> C (IN REF. 2).  
 FT CONFLICT 55 55 Q -> K (IN REF. 2).  
 FT CONFLICT 64 64 V -> A (IN REF. 2).  
 FT CONFLICT 145 145 P -> L (IN REF. 2).  
 SQ SEQUENCE 266 AA; 30717 MW; BDE07B58224AB78 CRC64;  
  
 Query Match 20.9%; Score 173.5; DB 1; Length 266;  
 Best Local Similarity 30.8%; Pred. No. 9e-11;  
 Matches 48; Conservative 27; Mismatches 62; Indels 19; Gaps 4;  
  
 QY 2 EKALKIDTPQOGSIQDINHRVWVLODQTLLAIVPRKDEMSPTIALISCRHVTLEKDRGN 61  
 DB 128 QKSLVLDSP-----CVLK---ALHLPQSEMSREVWFCM---SFVQGEERDNKI 169  
  
 QY 62 PLYLGLNGLCLMCAKVGDOPTLQLEKIDIMLYNOPEPVKSFLEYHSQSGRNSTFESV 121  
 DB 170 PVALGIRKDNLYLSCVKKGDPTLQLEVD-PKVYPRNMEKRFVYFKTEIKNTVEFESV 228

[illegible]

QY 15 IODINHRVWVLODQTLIA-----VPRKDRMSPVTIALISCRHVTLEKDRGNPIYLGL 67  
 Db 40 IWDVQKTFYLRNNQVAGYLOGPNKLEERIDVPL-----EPQLFLGI 85  
 QY 68 NGLNLCMLCAKVGDOPTLQLEKEDIMLYNQPEPVKSFYHSHSGRNSTFESVAFPGWF 127  
 Db 86 QRGKLCCLCKVSGDKMKLHLEAVNITDLGKNKEQDKRFTFIRSNSTGPTTTFESACPGWF 145  
 QY 128 IAVSEGGCPILLTQELGKANTTD 151  
 Db 146 ICTALEADQPVSLT-----NTPD 163

RESULT 9  
 IL1B\_CEREL  
 ID IL1B\_CEREL STANDARD; PRT; 266 AA.  
 AC P51745;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-1 beta precursor (IL-1 beta).  
 GN IL1B.  
 OS Cervus elaphus (Red deer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;  
 OC Cervidae; Cervinae; Cervus.  
 OX NCBI\_TaxID=9860;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lockhart E.A.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES. IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION AND PROLIFERATION, AND FIBROBLAST GROWTH FACTOR  
 CC ACTIVITY. IL-1 IS INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS  
 CC (BY SIMILARITY).  
 CC -!- SUBUNIT: MONOMER (By similarity).  
 CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS  
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
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 CC -----  
 CC EMBL; U20500; AAA62234.1; -  
 CC HSSP; P01584; 1H1B.  
 DR InterPro; IPR002348; IL1\_HBGF  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR InterPro; IPR003502; Interleukin\_1\_prop.  
 DR Pfam; PF00340; IL1; 1.  
 DR Pfam; PF02394; IL1\_HBGF.  
 DR PRINTS; PR00262; IL1\_HBGF.  
 DR ProDom; PD002536; Interleukin\_1; 1.  
 DR SMART; SM00125; IL1; 1.  
 DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
 KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.  
 FT PROPEP 1 113 BY SIMILARITY.  
 FT CHAIN 114 266 INTERLEUKIN-1 BETA.  
 SQ SEQUENCE 266 AA; 30629 MW; 4F0B4E6F09F060 CRC64;

Query Match

20.1%; Score 167; DB 1; Length 266;

Best Local Similarity 31.4%; Pred. No. 4 3e-10;  
 Matches 49; Conservative 25; Mismatches 64; Indels 18; Gaps 5;

QY 14 SIODINHRVWVLODQ-----TLIAVP-----RKDRMSPVTIALISCRHVTLEKDRGN 61  
 Db 115 AVQSVNCK---LQDREQNSLVASPKVLKALHLLSQMSREVVFCKM--FVQAEERDNKI 169  
 QY 62 PIVLGLNGLNLCMLCAKVGDOPTLQLEKEDIMLYNQPEPVKSFYHSHSGRNSTFESV 121  
 Db 170 FVALGIRDKNOYLSVCKKGGDTPTLQLEEDV-PKVYPRKNMEKRFVFKYTKIDTVEFESV 228  
 QY 122 AFGWFIIVSSEGGCPILLTQELGKANTTDGLTML 157  
 Db 229 LYPNWYISTSHPEKPVFLGHFRGGQDITDFRMETL 264

RESULT 10  
 IL1B\_BOVIN  
 ID IL1B\_BOVIN STANDARD; PRT; 266 AA.  
 AC P09478;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Interleukin-1 beta precursor (IL-1 beta).  
 GN IL1B.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89016591; PubMed=3262866;  
 RA Leong S.R., Flagg G.M., Lawman M., Gray P.W.;  
 RT "The nucleotide sequence for the cDNA of bovine interleukin-1 beta.";  
 RL Nucleic Acids Res. 16:9054-9054(1988).  
 CC -!- SUBUNIT: MONOMER (By similarity).  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES. IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION AND PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS  
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
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 CC -----  
 CC EMBL; M35589; AAA30585.1; -  
 CC EMBL; X12498; CAA31018.1; -  
 CC EMBL; M37211; AAA30584.1; -  
 CC PIR; JLO010; ICB01B.  
 CC PIR; S01380; S01380.  
 CC HSSP; P01584; 1H1B.

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DR InterPro: IPR002348; ILL_HBGF.
DR InterPro: IPR000975; Interleukin_1.
DR InterPro: IPR003502; Interleukin_1_prop.
DR Pfam: PF00340; ILL_1.
DR Pfam: PF02394; ILL_propep; 1.
DR PRINTS: PR00262; ILL_HBGF.
DR PRODOM: PD002536; Interleukin_1.
DR SMART: SM00125; ILL_1.
DR PROSITE: PS00253; INTERLEUKIN_1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 113
FT CHAIN 114 266 INTERLEUKIN-1 BETA.
FT CONFLICT 252 252 A -> G (IN REF. 2).
SQ SEQUENCE 266 AA; 30774 MW; 9D1EF8F57070586 CRC64;

Query Match 19.8%; Score 164; DB 1; Length 266;
Best Local Similarity 31.0%; Pred. No. 8.8e-10;
Matches 48; Conservative 23; Mismatches 76; Indels 8; Gaps 4;

QY 8 DTPOQG---SIQDINHRVWVLDQDTLIAVPR--KDRMSPVTIALISCRHVETLEKDRGNP 62
DB 113 DAPVQSTKCLQDRQKSLVSPCLVLAHLLSQEMNREVFCMS--FVQGEERDNKIP 170

QY 63 IYLGNGNLCLMCAKVGDDPTQLQKEKDIMLYNQPEPVKSFLYHSGRNSTFESVA 122
DB 171 VALGIKDKNLVLCVKGDDPTQLQLEVD--PKVYPRKNMEKREVFYKTEIKNTVFESVL 229

QY 123 FPGWFIASVSGGCPILITQELGKANTTDFGLTML 157
DB 230 YPNWYISTQIEERPVELGHFRAGQDITDFRMTL 264

RESULT 11
IL1B_CAPH1
ID IL1B_CAPH1 STANDARD; PRT; 266 AA.
AC P79162;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN IL1B.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Takakura H., Hashimoto O., Mori Y., Tatsumi M.;
RT "Molecular cloning and expression of caprine IL-1alpha and
RT IL-1beta.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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CC -----
DR EMBL: D63351; BAA09675.1; -.
DR HSSP: P01584; IHLB.
DR InterPro: IPR002348; ILL_HBGF.
DR InterPro: IPR000975; Interleukin_1.
DR InterPro: IPR003502; Interleukin_1_prop.
DR Pfam: PF00340; ILL_1.
DR Pfam: PF02394; ILL_propep; 1.
DR PRINTS: PR00262; ILL_HBGF.
DR PRODOM: PD002536; Interleukin_1.
DR SMART: SM00125; ILL_1.
DR PROSITE: PS00253; INTERLEUKIN_1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 113 BY SIMILARITY.
FT CHAIN 114 266 INTERLEUKIN-1 BETA.
FT CONFLICT 252 252 A -> G (IN REF. 2).
SQ SEQUENCE 266 AA; 30769 MW; 59F7B39BD1D4DDA5 CRC64;

Query Match 19.6%; Score 162.5; DB 1; Length 266;
Best Local Similarity 31.4%; Pred. No. 1.3e-09;
Matches 49; Conservative 25; Mismatches 63; Indels 19; Gaps 4;

QY 2 EKALKIDTPQGSIQDINHRVWVLDQDTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
DB 128 QKSLVLDSP-----CVLKALHLLS---QEMSRREVFCMS--FVQGEERDNKI 169

QY 62 PIYLGNGNLCLMCAKVGDDPTQLQKEKDIMLYNQPEPVKSFLYHSGRNSTFESV 121
DB 170 PVALGIRDKNLYLSWVKKGDDPTQLQLEVD--PKVYPRKNMEKREVFYKTEIKNTVFESV 228

QY 122 APFGWFIASVSGGCPILITQELGKANTTDFGLTML 157
DB 229 LYPNWIYSTQIEERPVELGHFRAGQDITDFRMTL 264

RESULT 12
IL1B_PIG
ID IL1B_PIG STANDARD; PRT; 267 AA.
AC P26889;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN IL1B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93314575; PubMed=8325511;
RA Huecher M.J., Lin G., Smith D.M., Murtaugh M.P., Mollitor T.W.;
RT "Cloning, sequencing and regulation of an mRNA encoding porcine
RT interleukin-1 beta.";
RL Gene 129:285-289(1993).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----

```



CC THE RELEASE OF PROTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
CC -!- SUBUNIT: MONOMER.  
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDERINED FUNCTION.  
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS  
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
CC SECRETORY PROTEINS.  
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U19845; AAA86709.1; .  
DR HSSP; P01584; 1H1B.  
DR InterPro; IPR002348; IL1\_HBGF.  
DR InterPro; IPR000975; Interleukin\_1.  
DR InterPro; IPR003502; Interleukin\_1\_prop.  
DR Pfam; PF00340; IL1; 1.  
DR PRINTS; PR002394; IL1\_propep; 1.  
DR ProDom; PD002536; Interleukin\_1; 1.  
DR SMART; SM00125; IL1; 1.  
DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.  
FT PROPEP 1 116 BY SIMILARITY.  
FT CHAIN 117 269 INTERLEUKIN-1 BETA.  
SQ SEQUENCE 269 AA; 30481 MW; A7CD59EBAC120EC7 CRC64;

Query Match 17.5%; Score 145.5; DB 1; Length 269;

Best Local Similarity 34.5%; Pred. NO. 7.5e-08;

Matches 39; Conservative 15; Mismatches 56; Indels 3; Gaps 2;

QY 46 LISCRHVTLEKDRGNPIYGLNGNLCLMCAKVGDOPTLOLKEKDMDLYNQPEPKSF 105

Db 157 VFSMSVQGEESNDKIPVALGKANKLYLSCVLKDDKPTQLQLESVDPRN-YPKKMEKRF 215

QY 106 LFVHSQSGRNSTFESVAFPGFWFIASVSGGCPILITQELGKANTDFGLTMLF 158

Db 216 VFNKIEINKLFESAQFPNWISTSAENMPVFLGGTRGGDITDF--TMQF 266

#### RESULT 15

ID IL1B\_HUMAN STANDARD; PRT; 269 AA.  
AC P01584; O96HE5; O9UCP6;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Interleukin-1 beta precursor (IL-1 beta) (Catabolin).  
GN IL1B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85088517; PubMed=6083565;  
RA Auron P.E., Webb A.C., Rosenwasser L.J., Mucci S.F., Rich A.,  
RA Wolff S.M., Dinarello C.A.;  
RT "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:7907-7911(1984).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85240547; PubMed=2989698;  
RA March C.J., Mosley B., Larsen A., Cerretti D.P., Braedt G., Price V.,  
RA Gillis S., Henney C.S., Kronheim S.R., Grabstein K., Conlon P.J.,

RA Hopp T.P., Cosman D.;  
RT "Cloning, sequence and expression of two distinct human interleukin-1  
RT complementary DNAs.";  
RL Nature 315:641-647(1985).  
[3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87040762; PubMed=3490654;  
RA Clark B.D., Collins K.L., Gandy M.S., Webb A.C., Auron P.E.;  
RT "Genomic sequence for human prointerleukin 1 beta: possible evolution  
RT from a reverse transcribed prointerleukin 1 alpha gene.";  
RL Nucleic Acids Res. 14:7897-7914(1986).  
[4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87248099; PubMed=2954882;  
RA Bensi G., Raugel G., Pallia E., Carinci V., Buonamassa D.T., Melli M.;  
RT "Human interleukin-1 beta gene.";  
RL Gene 52:95-101(1987).  
[5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90249285; PubMed=2635664;  
RA Kotenko S.V., Bulenkov M.T., Veiko V.P., Epishin S.M., Lomakin I.B.,  
RA Emel'yanov A.V., Kozlov A.P., Konusova V.G., Kotov A.Y.,  
RA Kurbatova T.V., Reshetnikov V.L., Simbirtsev A.S., Ketlinskii S.A.,  
RA Vinetskii Y.P.;  
RT "Cloning of the cDNA coding for human prointerleukin-1 alpha and  
RT prointerleukin-1 beta.";  
RL Dokl. Akad. Nauk SSSR 309:1005-1008(1989).  
[6]  
RP SEQUENCE FROM N.A.  
RA Webb A.C., Dinarello C.A., Rosenwasser L.J., Mucci S.F., Rich A.,  
RA Wolff S.M., Auron P.E.;  
RT "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";  
RL Adv. Gene Technol. 22:339-340(1985).  
[7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87156769; PubMed=3493774;  
RA Nishida T., Nishino N., Takano M., Kawai K., Bando K., Masui Y.,  
RA Nakai S., Hirai Y.;  
RT "cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell  
RT line.";  
RL Biochem. Biophys. Res. Commun. 143:345-352(1987).  
[8]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
[9]  
RP SEQUENCE OF 117-128.  
RX MEDLINE=88184226; PubMed=3281727;  
RA Zsebo K.M., Wypych J., Yuschenskoff V.N., Lu H., Hunt P., Dukes P.P.,  
RA Langley K.E.;  
RT "Effects of hematopoietin-1 and interleukin 1 activities on early  
RT hematopoietic cells of the bone marrow.";  
RL Blood 71:962-968(1988).  
[10]  
RP SEQUENCE OF 114-135.  
RC TISSUE=Skin;  
RX MEDLINE=92013781; PubMed=1919436;  
RA Mizutani H., Schechter N., Lazarus G., Black R.A., Kupper T.S.;  
RT "Rapid and specific conversion of precursor interleukin 1 beta (IL-1  
RT beta) to an active IL-1 species by human mast cell chymase.";  
RL J. Exp. Med. 174:821-825(1991).  
[11]  
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
RX MEDLINE=88211543; PubMed=3259176;  
RA Priestle J.P., Schar H.-P., Grutter M.G.;  
RT "Crystal structure of the cytokine interleukin-1 beta.";  
RL EMBO J. 7:339-343(1988).  
[12]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=90093925; PubMed=2602367;  
RA Priestle J.P., Schar H.-P., Grutter M.G.;  
RT "Crystallographic refinement of interleukin 1 beta at 2.0-A

RT resolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9667-9671(1989).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=90064532; PubMed=2585509;  
 RA Finzel B.C., Clancy L.L., Holland D.R., Muchmore S.W.,  
 RA Watenpugh K.D., Einspahr H.M.;  
 RT "Crystal structure of recombinant human interleukin-1 beta at 2.0-A  
 resolution.";  
 RL J. Mol. Biol. 209:779-791(1989).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH RECEPTOR.  
 RX MEDLINE=97215903; PubMed=9062193;  
 RA Vigers G.P., Anderson L.J., Caffes P., Brandhuber B.J.;  
 RT "Crystal structure of the type-I interleukin-1 receptor complexed  
 with interleukin-1beta";  
 RL Nature 386:190-194(1997).  
 RN [15]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=90321925; PubMed=2372550;  
 RA Driscoll P.C., Gronenborn A.M., Wingfield P.T., Clore G.M.;  
 RT "Determination of the secondary structure and molecular topology of  
 interleukin-1 beta by use of two- and three-dimensional heteronuclear  
 15N-1H NMR spectroscopy.";  
 RL Biochemistry 29:4668-4682(1990).  
 RN [16]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=91159409; PubMed=2001363;  
 RA Clore G.M., Wingfield P.T., Gronenborn A.M.;  
 RT "High-resolution three-dimensional structure of interleukin 1 beta in  
 solution by three- and four-dimensional nuclear magnetic resonance  
 spectroscopy.";  
 RL Biochemistry 30:2315-2323(1991).  
 CC -|- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
 THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
 CC -|- SUBUNIT: MONOMER.  
 CC -|- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -|- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS  
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -|- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M15840; AAA74137.1; -;  
 DR EMBL: X02532; CAA26372.1; -;  
 DR EMBL: K02770; AAA36106.1; -;  
 DR EMBL: X04500; CAA28185.1; -;  
 DR EMBL: X56087; CAA39567.1; -;  
 DR EMBL: M54933; AAA59136.1; -;  
 DR EMBL: M15330; AAA59135.1; -;  
 DR EMBL: BC008678; AAH08678.1; -;  
 DR PIR: A01848; ICHU1B.  
 DR PIR: A25542; A25542.  
 DR PIR: A29019; A29019.  
 DR PIR: B27616; B27616.  
 DR PIR: S19626; S19626.  
 DR PDB: 111B; 15-OCT-92.  
 DR PDB: 211B; 15-JUL-93.  
 DR PDB: 411B; 15-JAN-93.  
 DR PDB: 511B; 15-OCT-94.

DR PDB: 611B; 15-OCT-92.  
 DR PDB: 711B; 15-OCT-92.  
 DR PDB: 211B; 15-APR-92.  
 DR PDB: 311B; 15-APR-92.  
 DR PDB: 411B; 15-JUL-92.  
 DR PDB: 111B; 31-JAN-94.  
 DR PDB: 110B; 17-AUG-96.  
 DR PDB: 117B; 04-FEB-98.  
 DR PDB: 911B; 06-JAN-99.  
 DR MIM: 147720; -;  
 DR InterPro: IPR002348; IL1\_HBGF.  
 DR InterPro: IPR000975; Interleukin\_1.  
 DR InterPro: IPR003502; Interleukin\_1\_prop.  
 DR Pfam: PF00340; IL1; 1.  
 DR Pfam: PF02394; IL1\_propep; 1.  
 DR PRINTS; PR00262; IL1HBGF.  
 DR ProDom; PD002336; Interleukin\_1; 1.  
 DR SMART; SM00125; IL1; 1.  
 DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
 DR KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;  
 KW 3D-structure.  
 FT PROPEP 1 116  
 FT CHAIN 117 269 INTERLEUKIN-1 BETA.  
 FT CONFLICT 6 6 K -> E (IN REF. 2, 6 AND 8).  
 FT CONFLICT 20 20 D -> H (IN REF. 7).  
 FT CONFLICT 111 111 E -> Q (IN REF. 7).  
 FT CONFLICT 177 177 G -> A (IN REF. 7).  
 FT CONFLICT 214 214 R -> P (IN REF. 7).  
 FT STRAND 121 128  
 FT TURN 129 130  
 FT STRAND 132 138

Query Match 17.3%; Score 143.5; DB 1; Length 269;

Best Local Similarity 34.5%; Pred. NO. 1.2e-07;

Matches 39; Conservative 15; Mismatches 56; Indels 3; Gaps 2;

QY 46 LISCRHVETLEKDRGNPIVLGNLNLCLMCAKVGDPQLQLKEKDMDLYNQPEPVKSF 105

Db 157 VFSMSFVQGESNDKTPVALGLKERNLYLSCVLKDDKPTLQLESVDPKN-YPKKKMEKRF 215

QY 106 LFHVSQSRNSTESVAFPGWFIAVSSEGGCPILITQLGLKANTDTGLTMLF 158

Db 216 VFNKIEINNKLEFSAQFPNWYISTSAQENMPVFLGGTKGGDITDF--TMOF 266

Search completed: June 20, 2002, 15:11:20

Job time: 445 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 20, 2002, 15:10:54 ; Search time 61.16 Seconds  
(without alignments) 446.913 Million cell updates/sec

Title: US-09-763-498-8  
 Perfect score: 830  
 Sequence: 1 MEKALKIDTPQGSIQDINH.....ILTOELGKANTDFGLTMLF 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100%

**Listing first 45 summaries**

Database :

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1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.mhc.*
8: sp.organelle.*
9: sp.phage.*
10: sp.plant.*
11: sp.podent.*
12: sp.virus.*
13: sp.vertibrate.*
14: sp.unclassified.*
15: sp.virus.*
16: sp.bacteriap.*
17: sp.archaeap.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	830	100.0	158	4	Q9UHA7	Q9UHA7	homo sapien
2	466.5	56.2	169	4	Q9NZH8	Q9NZH8	homo sapien
3	463	55.8	160	11	Q9JLA2	Q9JLA2	mus musculus
4	385	46.4	157	4	Q9UHA5	Q9UHA5	homo sapien
5	333	40.1	183	11	Q9D6Z6	Q9D6Z6	mus musculus
6	209	25.2	192	4	Q9UHA6	Q9UHA6	homo sapien
7	209	25.2	218	4	Q9NZH6	Q9NZH6	homo sapien
8	209	25.2	218	4	Q9HBF3	Q9HBF3	homo sapien
9	202	24.3	164	4	Q9NZH7	Q9NZH7	homo sapien
10	185.5	22.3	155	4	Q9UBH0	Q9UBH0	homo sapien
11	185	22.3	267	13	Q73909	Q73909	gallus gallus
12	183.5	22.1	159	4	Q96GD6	Q96GD6	homo sapien
13	180.5	21.7	176	6	Q9BEH0	Q9BEH0	canis famill
14	172.5	20.8	177	6	Q9GMZ4	Q9GMZ4	tursiops tr
15	170.5	20.5	176	6	Q9GKK2	Q9GKK2	canis famill
16	169	20.4	152	4	Q969H5	Q969H5	homo sapien

## ALIGNMENTS

```

RESULT 1
Q9UHA7          Q9UHA7          PRELIMINARY;      PRT;    158 AA.
ID Q9UHA7;
AC Q9UHA7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FILI EPSILON.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20092888; PubMed=10635660;
RX Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily." ;
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL; AF201831; AAF25211.1; -.
DR HSPG; P18510; IILR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;

Query Match          100.0%; Score 830; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKALKIDTPOQGSIQDINHRVWVLDQDTLIAVPRKDRMSPTVIALISCRHVETLEKDRG 60
   |||||
Db 1 MEKALKIDTPOQGSIQDINHRVWVLDQDTLIAVPRKDRMSPTVIALISCRHVETLEKDRG 60
   |||||

QY 61 NPIYGLNGLNCLMCAKVGDDPTQLQEKDIDMLYNQPEPVKSFLEYHSGSGRNSTFES 120
   |||||
Db 61 NPIYGLNGLNCLMCAKVGDDPTQLQEKDIDMLYNQPEPVKSFLEYHSGSGRNSTFES 120
   |||||

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QY 121 VAFPGWFIATVSEGGCPILITQELGKANTTDFGLTMLF 158  
DB 121 VAFPGWFIATVSEGGCPILITQELGKANTTDFGLTMLF 158

## RESULT 2

ID Q9NZH8 PRELIMINARY; PRT; 169 AA.  
AC Q9NZH8;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-DEC-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON).  
GN IL1E.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=20209405; PubMed=10744718;  
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,  
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,  
RA Young P.R.;  
RT "Identification and initial characterization of four novel members of  
the interleukin-1 family.";  
RL J. Biol. Chem. 275:10308-10314(2000).  
RN [2]  
SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J; TISSUE=EMBRYO;  
MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL; AF200493; AAF69249.1; -;  
DR EMBL; AF206697; AAG35671.1; -;  
DR EMBL; AK004061; BAB23147.1; -;  
DR HSSP; P01584; 1H1B.  
DR MGD; MGI:1859324; I11f6.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
DR ProDom; PD002536; Interleukin\_1; 1.  
DR SMART; SM00125; IL1; 1.  
SQ SEQUENCE 169 AA; 18721 MW; F00A9243706F4154 CRC64;

Query Match 56.2%; Score 466.5; DB 4; Length 169;  
Best Local Similarity 59.9%; Pred. No. 1.9e-42;  
Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;

QY 10 PQGSIQDINHVRVVLQDQTLIAVPRKDRMSPTIALISCRHVETLEKDRGNPIYLGLNG 69  
DB 22 PITGTLNDLNNQVWTLQGNLVAVPRSDSVPTVAVITCKYPEALEQGRGDPVILGIGN 81

QY 70 LNLCLCAKVGDDPTQLKEKIDMDLYNQPEPVKSFLEFVHSQSGRNSTPESVAFPGWFI 129  
DB 82 PEMCLYCEKVGQEQTLQLEKIDMDLYNQPEPVKPFLEFRAGTKRTSTLESVAFPDWFI 141

QY 130 VSSEGCPLLTQELGKANTTDFGLTM 156

DB 142 -SSKRDQPIILTSLEKSNYAFELNI 167

## RESULT 3

ID Q9JLA2 PRELIMINARY; PRT; 160 AA.  
AC Q9JLA2;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON).  
GN IL1F6 OR FIL1 OR IL1E.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=20209405; PubMed=10744718;  
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,  
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,  
RA Young P.R.;  
RT "Identification and initial characterization of four novel members of  
the interleukin-1 family.";  
RL J. Biol. Chem. 275:10308-10314(2000).  
RN [2]  
SEQUENCE FROM N.A.  
RX Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;  
RT "Novel IL-1 family member IL-1e responds through the orphan IL-1R-  
related protein 2; response is antagonized by IL-1d.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J; TISSUE=EMBRYO;  
MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL; AF200493; AAF69249.1; -;  
DR EMBL; AF206697; AAG35671.1; -;  
DR EMBL; AK004061; BAB23147.1; -;  
DR HSSP; P01584; 1H1B.  
DR MGD; MGI:1859324; I11f6.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
DR ProDom; PD002536; Interleukin\_1; 1.  
DR SMART; SM00125; IL1; 1.  
SQ SEQUENCE 160 AA; 18015 MW; AA0434D68FF62F4A CRC64;

Query Match 55.8%; Score 463; DB 11; Length 160;  
Best Local Similarity 54.5%; Pred. No. 4.2e-42;  
Matches 85; Conservative 30; Mismatches 41; Indels 0; Gaps 0;

QY 2 EKALKIDTPQGGSTQDINHVRVVLQDQTLIAVPRKDRMSPTIALISCRHVETLEKDRGN 61  
DB 4 EKELRAASPSLRHVQDLSSRVILQNNILTAAPRKEQTPVTITLLPCQYLDLTETNRGD 63

QY 62 PIYGLNGLNLCMLCAKVGDDPTQLKEKIDMDLYNQPEPVKSFLEFVHSQSGRNSTPESV 121  
DB 64 PTYMGVQRPMSCLFCTKDGQEPVLQEGNIMWNTNKEPVKASLFYHKSGTSTTESA 123

QY 122 APFGWFIATVSEGGCPILITQELGKANTTDFGLTML 157

DB 124 APFGWFIATVSEGGCPILITQELGKANTTDFGLTML 159

RESULT 4  
Q9UHA5

[illegible]

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Db 89 KGFECLYCDKQSGSPSLQKELMLAAQKESARRPFIFYRAQVGSWNMLESAHPG 148
QY 126 WFIATVSEGGCPILITQELGKANTTDF 152
Db 149 WFICTSCNCEPVGVTDFKFNKKHIEF 175

RESULT 7
Q9NZH6 PRELIMINARY; PRT; 218 AA.
AC Q9NZH6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN-1 HOMOLOG 4 (IL-1X PROTEIN) (INTERLEUKIN-1-RELATED PROTEIN
DE LONG ISOFORM A).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066552; PubMed=11145836;
RA Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
[2]
RP SEQUENCE FROM N.A.
RX TISSUE-PETAL LUNG, FETAL TESTIS, FETAL B-CELL, AND FETAL COLON;
RX MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
[2]
RP SEQUENCE FROM N.A.
RX TISSUE-COLON CARCINOMA;
RA Manoj P.P., Mantovani A., Muzio M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Yansura D.,
RA Lewis L., Eigenbrot C., Henzel W.J., Vandlen R., Filvaroff E.;
RT "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-
RT 1Rrp.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF200496; AAF69252.1; -
DR EMBL; AF167368; AAG29344.1; -
DR EMBL; AF251116; AAG14420.1; -
DR HSSP; P18510; ILIR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 218 AA; 24126 MW; 96E089310D2CEA68 CRC64;

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Query Match 25.2%; Score 209; DB 4; Length 218;
Best Local Similarity 36.7%; Pred. No. 1.5e-14;
Matches 54; Conservative 26; Mismatches 61; Indels 6; Gaps 4;

QY 10 PQGSGTODINHRVWVLDQDTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGNPIYLGLN 68
Db 57 PKFSIHQDHQKVLVLDGSLNLIAPVDKNYIRPEIFFALAS--SLSSASAEKSGPILLGVS 114
QY 69 GLNLCLMCAKVGQD--PTLQLEKIDMDLYNQPEPV-KSFLFYHSQSGRNSTFESVAFPG 125
Db 115 KGFECLYCDKQSGSPSLQKELMLAAQKESARRPFIFYRAQVGSWNMLESAHPG 174

RESULT 8
Q9HBF3 PRELIMINARY; PRT; 218 AA.
AC Q9HBF3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN-1-RELATED PROTEIN LONG ISOFORM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-OSTEOCLASTOMA;
RX MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
DR EMBL; AF200494; AAF69250.1; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 164 AA; 18521 MW; F0D2099F4A357A0A CRC64;

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Query Match 24.3%; Score 202; DB 4; Length 164;
Q9HBF3

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ID Q9HBF3 PRELIMINARY; PRT; 218 AA.
AC Q9HBF3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN-1-RELATED PROTEIN LONG ISOFORM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066552; PubMed=11145836;
RA Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
RA Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.,
RA "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
RT 1Rrp.";
RL Cytokine 13:1-7(2001).
DR EMBL; AF251119; AAG14421.1; -
DR HSSP; P18510; ILIR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 218 AA; 24138 MW; 76E09C35093DEA63 CRC64;

Query Match 25.2%; Score 209; DB 4; Length 218;
Best Local Similarity 36.7%; Pred. No. 1.5e-14;
Matches 54; Conservative 26; Mismatches 61; Indels 6; Gaps 4;

QY 10 PQGSGTODINHRVWVLDQDTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGNPIYLGLN 68
Db 57 PKFSIHQDHQKVLVLDGSLNLIAPVDKNYIRPEIFFALAS--SLSSASAEKSGPILLGVS 114
QY 69 GLNLCLMCAKVGQD--PTLQLEKIDMDLYNQPEPV-KSFLFYHSQSGRNSTFESVAFPG 125
Db 115 KGFECLYCDKQSGSPSLQKELMLAAQKESARRPFIFYRAQVGSWNMLESAHPG 174

QY 126 WFIATVSEGGCPILITQELGKANTTDF 152
Db 175 WFICTSCNCEPVGVTDFKFNKKHIEF 201

RESULT 9
Q9NZH7 PRELIMINARY; PRT; 164 AA.
ID Q9NZH7
AC Q9NZH7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-1 HOMOLOG 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-OSTEOCLASTOMA;
RX MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
DR EMBL; AF200494; AAF69250.1; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 164 AA; 18521 MW; F0D2099F4A357A0A CRC64;

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QY	10	POGSIODINHRRVWLQDOTLIAPRKORMSPTVLTJLISCHVETLEKDRGNPIYVLGNG	69
Db	9	PKSYAIRDSRQMWVLSNGSLTAAPLSIRKIPVTUHLTIACRDTFSDKEKGNMVLGIKG	68
QY	70	LNLCMLCAKVGDPITQLKEKDMD	94
Db	69	KDCLCFCAEIOGKPTQLKLGQSQD	93
RESULT	10		
Q9UBHO		PRELIMINARY;	PRT; 155 AA.
AC	Q9UBHO		
DT	01-MAY-2000	(TREMBLrel. 13, Created)	
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	
DT	01-OCT-2001	(TREMBLrel. 18, Last annotation update)	
DE	FILL DELTA	(INTERLEUKIN-1 LIKE PROTEIN 1) (INTERLEUKIN-1 RECEPTOR	
DE	ANTAGONIST HOMOLOG 1)	(INTERLEUKIN-1 DELTA).	
GN	IL1H1 OR IL1L1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa;		
OC	Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20092888; PubMed=10625660;		
RA	Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,		
RA	Sing J.E.;		
RT	"Four New Members Expand the IL-1 Superfamily.";		
RL	J. Biol. Chem. 275:1169-1175(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99443727; PubMed=10512743;		
RA	Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,		
RA	Dmanac R., Ford J.E.;		
RT	"IL1H1: A Novel Interleukin-1 Receptor Antagonist Gene.";		
RL	Biochem. Biophys. Res. Commun. 263:702-706(1999).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PLACENTA;		
RA	Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.;		
RT	"A tissue specific interleukin-1 receptor antagonist homolog from the		
RT	ILI cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RA	Barton J.L., Herbst R., Bostisio D., Nicklin M.J.H.;		
RT	"A tissue specific interleukin-1 receptor antagonist homolog from the		
RT	IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20322477; PubMed=10866108;		
RA	Mulero J.J., Nelken S.T., Ford J.E.;		
RT	"Organization of the Human Interleukin-1 Receptor Antagonist Gene		
RT	IL1H1.";		
RL	Immunogenetics 51:425-428(2000).		
RN	[6]		
RP	SEQUENCE FROM N.A.		
RA	Debets R., Timans R.A.		
RT	"Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";		
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF201830; AAF25210.1;		
DR	EMBL; AF186094; AAF02757.1;		
DR	EMBL; AJ242737; CAB59822.1;		
DR	EMBL; AJ242738; CAB59823.1;		
DR	EMBL; AJ271338; CAB67704.1;		
DR	EMBL; AF216693; AAF76981.1;		
DR	EMBL; AF230377; AAF91274.1;		

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DR PROSITE: PS00253; INTERLEUKIN_1; 1.
KW Receptor.
SQ SEQUENCE 177 AA; 19923 MW; 6FD19A06C09B131B CRC64;

Query Match 15 IQDINHRRVVVLDQDTLIA-----VPRKDRMSPTVIALISCRHVETLEKDRGNPIYLGL 67
      1 1 1 : : : : 1 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Best Local Similarity 31.3%; Pred. No. 1e-10;
Matches 42; Conservative 24; Mismatches 47; Indels 21; Gaps

Qy 15 IQDINHRRVVVLDQDTLIA-----VPRKDRMSPTVIALISCRHVETLEKDRGNPIYLGL 67
Db 40 IWDVNQKTFYLRNNOLVAGYLGQPNTKLEEKIDVVPI-----EPHMFGLI 85

Qy 68 NGLNLCILCMKAVGDQPTTLQLKEKDIMDLYNOPEPKYKSLFYHSQSGRNSTFESVAFPGWF 127
      : 1 1 1 1 1 1 1 1 1 1 : : : : : : : : : : : : : : : : : : : : : :
Db 86 HGGKLCACVKSQDEIKLGLPEVNTIDLNSSKEEDKREAFIRSDSGPTTFSESAACPGWF 145

Qy 128 IAVSSEGGCPILLT 141
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 146 LCTALETDQPVGLT 159

RESULT 15
Q9GKK2 ID Q9GKK2 PRELIMINARY; PRT: 176 AA.
AC Q9GKK2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

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Search completed: June 20, 2002, 15:10:54  
Job time: 465 sec



GenCore version 4.5  
Copyright (C) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 11:56:23 ; Search time 2781.56 Seconds  
(without alignments)  
3588.619 Million cell updates/sec

Title: US-09-763-498-12

Perfect score: 477  
Sequence: 1 atggaaaagcattgaaat.....ggtaactatgctgttttaa 477

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pi.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pi.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htgO\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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1	475.4	99.7	477	9	AF201831
2	349.8	73.3	391	6	AX193589
3	238.6	50.0	483	10	AF200493
4	238.6	50.0	795	10	AF206697
5	222	46.5	244	6	AX193660
6	215.8	45.2	197308	9	AC016724
7	202	42.3	1073	6	AX207820
8	202	42.3	1177	9	AF206696
9	202	42.3	1183	6	E54910
10	202	42.3	1183	9	AF200492
11	134.2	28.1	520	6	AX193587
12	134.2	28.1	585	6	AX052581
13	134.2	28.1	585	9	AF201833
14	134.2	28.1	1244	6	AX167128
15	129.2	27.1	746	6	AR137703
16	127	26.6	243	6	AR137705
17	127	26.6	294	6	AR137704
18	112	23.5	329	6	AX193643
19	106.4	22.3	186587	2	AC106686
20	79.4	16.6	184626	2	AC096974
21	78.8	16.5	1036	4	AY026462
22	77.2	16.2	563	4	AF216526
23	74.8	15.7	520	10	MUSILRA
24	74.8	15.7	542	10	S64082
25	74.8	15.7	604	10	AF001795
26	74.8	15.7	1576	10	MUSILRAA
27	74.8	15.7	1877	6	E55194
28	74.8	15.7	1877	10	MUSILRN
29	74.8	15.7	1940	10	MUSILRA
30	71.8	15.1	531	6	AX127225
31	71.8	15.1	603	6	AX127227
32	71.8	15.1	1590	4	D83714
33	71.8	15.1	1590	6	E15594
34	71.8	15.1	1614	4	ECU92482
35	71.8	15.1	1614	6	AX127224
36	71.2	14.9	197308	9	AC016724
37	71	14.9	574	4	S68977
38	70.8	14.8	462	6	AR105636
39	70.8	14.8	474	6	A50276
40	70.8	14.8	474	6	AR001464
41	70.8	14.8	474	6	AR055509
42	70.8	14.8	474	6	AR085392
43	70.8	14.8	514	6	I42450
44	70.8	14.8	531	6	A49726
45	70.8	14.8	531	6	A50144

ALIGNMENTS

RESULT 1  
AF201831  
LOCUS AF201831 477 bp mRNA linear PRI 16-JAN-2000  
DEFINITION Homo sapiens F1L1 epsilon mRNA, complete cds.  
ACCESSION AF201831  
VERSION AF201831.1 GI:6694389  
KEYWORDS human.  
SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 477)

Smith,D.E., Renshaw,B.R., Ketchum,R.R., Kubin,M., Garka,K.E. and Sims,J.E.

Four new members expand the interleukin-1 superfamily

J. Biol. Chem. 275 (2), 1169-1175 (2000)

2 (bases 1 to 477)

Sims,J.E.

Direct Submission

Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51

University Street, Seattle, WA 98101, USA

Location/Qualifiers

FEATURES

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Best Local Similarity									96.5%; Pred.No. 6e-96;	
CDS										
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Qy	109	gacctgatgttccaagtaaatcttatattcaatcgcacatatgagacccttag	168							
Dd	61	G-----TGTTCCCAGTAACAATTGCCTTAATCTAATGCGGACATGTGGAGACCCTTAG	114							
Qy	169	aaagcacagggaaaaccccatctacatggcctgaatggactcaatcttgctgatgtgt	228							
Dd	115	AAGACAGAGGGAACCCCATCTACTCGGCTGAATGSAGTCAATCTCGCTGATGTGT	174							
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Dd	235	TGTACAACAACCCGAGCCTGTGAAGTCCTTTCTCTTCTTACCACAGCCAGAGTGGCAGG	294							
Qy	343	aactcaccttcagctgtggtctccccggctggctcagctcagctctaagga	402							
Dd	295	AACCTCACCTTCGAGTCTGTGCTTTCCCTGGCTGGTTTCATCGCTGTCAAGTCTGAAGGA	354							
Qy	403	ggctgtccttcattcttaccacgaagaactggggaag	439							
Dd	355	GGCTGTCTCTCATCTCTTACCACGAAGAACCTGGGGAAG	391							
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AF200493	LOCUS AF200493 Mus musculus interleukin-1 homolog l mRNA linear ROD 11-MAY-2000									
DEFINITION	Mus musculus interleukin-1 homolog l mRNA, complete cds.									
ACCESSION	AF200493									
VERSION	AF200493.1 GI:7769113									
KEYWORDS	house mouse,									
SOURCE	ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Eusarcophaginae; Soricomorpha; Cricetidae; Muridae; Murinae; Mus.; Mus musculus									
REFERENCE	Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N., Griswold,D.E., Cappier,E.A., Tai-Singer,R., Wells,G.I., Doyle,M.L. and Young,P.R.									
AUTHORS	Identification and initial characterization of four novel members of the interleukin-1 family									
JOURNAL MEDLINE	J. Biol. Chem. 275 (14), 10308-10314 (2000)									
PUBLISHED	20209405 10744718									
REFERENCE	2 (bases 1 to 483) Kumar,S., McDonnell,P.C. and Young,P.R.									
AUTHORS	Direct Submission									
TITLE	Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109, SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of Prussia, PA 19406, USA									
JOURNAL	Location/Qualifiers									
FEATURES	Source Location/Qualifiers 1..483 /organism="Mus musculus" /db_xref="taxon:10090" /cell_line="PAM 212" /cell_type="keratinocyte" 1..483									
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QY 1 atggaagaaagcattgaaatgacacacccctcagcg9gggagcattcaggatatacatcat 60  
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 QY 121 ccagtcactattgcttaactcgtccgacatgtgagacccttggagaagacagagg 180  
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 QY 181 aaccccatctacctgggctggaatggactcaatctgcctgtatgtgtctaaagtcggg 240  
 Db 187 GATCCACGTAATGAGGAGTGCAAGCGCATGAGCTGCCTGTCTGCACAAAGGATGGG 246  
 QY 241 gaccagccacatgcagctgaagaaagataatgattgtacacacacacagcag 300  
 Db 247 GAGCAGCCTGTGCTACAGCTTGGGGAAGGAACATAATGGAATGTACAAACAAAGGAA 306  
 QY 301 cctgtgaagtccttctctctaccagccagcagtgagtgaggagactccacttcgagtc 360  
 Db 307 CCTGTAAAGCCCTCTCTCTATACACAAAGAGTGGTACACCTCTCATTTGAGTCT 366  
 QY 361 gtgctttccctggctggttcagctgtcagctctgaaaggagcgtctcctcctcatctt 420  
 Db 367 GCAGCCTTCCTGGTGGTTCATCGCTGTCTCTAAAGGGAGTGCCTCCACTCAITCTG 426  
 QY 421 accaagaactgggaaagcacaactcagacttgggttaactatgctgttttaa 477  
 Db 427 ACCCAAGAACTGGGGGAAATCTTCATCACTGACTTCAGATGATGTGTGTTCAATAA 483

RESULT 4  
 AF206697 795 bp mRNA linear ROD 01-NOV-2001  
 LOCUS Mus musculus Interleukin-1 epsilon (Il1e) mRNA, complete cds.  
 DEFINITION AF206697.1 GI:11493849  
 VERSION  
 KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 795)  
 DeBets, R., Timans, J.C., Homey, B., Zurawski, S., Sana, T.R., Lo, S.,  
 Wagner, J., Edwards, G., Clifford, T., Menon, S., Bazan, J.F. and  
 Kastelein, R.A.  
 Two novel IL-1 family members, IL-1 delta and IL-1 epsilon,  
 function as an antagonist and agonist of NF-kappa B activation  
 through the orphan IL-1 receptor-related protein 2  
 J. Immunol. 167 (3), 1440-1446 (2001)  
 21359532  
 MEDLINE  
 11466363  
 PUBLISHED  
 2 (bases 1 to 795)  
 DeBets, R., Timans, J.C., Zurawski, S., Bazan, J.F. and Kastelein, R.A.

TITLE Direct Submission  
 JOURNAL Submitted (18-NOV-1999) Molecular Biology, DNAX Research Institute  
 of Molecular and Cellular Biology, Inc., 901 California Avenue,  
 Palo Alto, CA 94304-1104, USA  
 FEATURES  
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BASE COUNT 237 a 177 c 174 g 207 t  
 ORIGIN

Query Match 50.0%; Score 238.6; DB 10; Length 795;  
 Best Local Similarity 68.8%; Pred. No. 6.8e-62;  
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QY 1 atggaagaaagcattgaaatgacacacccctcagcg9gggagcattcaggatatacatcat 60  
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 QY 61 cgggtgtggtttctcaggacacagcgtcattagcagtcctcagcaggaagaccgtatgtct 120  
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 DEFINITION Sequence 82 from Patent WO0140291.  
 ACCESSION AX193660

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Best Local Similarity 99.1%; Pred. No. 1.2e-54;  
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AX207820 LOCUS 1073 bp DNA linear PAT 31-AUG-2001  
DEFINITION Sequence 3 from Patent WO0157219.  
ACCESSION AX207820  
VERSION AX207820.1 GI:15422467  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 1073)  
AUTHORS Debets,J.E., Timans,J.C., Bazan,J.F. and Kastelein,R.A.  
TITLE Mammalian interleukin-1-delta and -epsilon. Their use in therapeutic and diagnostic methods  
JOURNAL Patent: WO 0157219-A 3 09-AUG-2001;  
FEATURES SCHERING CORPORATION (US)  
source Location/Qualifiers  
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67. .576 CDS



SOURCE	unidentified.
ORGANISM	unidentified.
REFERENCE	1 (bases 1 to 1183)
AUTHORS	Peter,R.Y.
TITLE	Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide
JOURNAL	Patent: JP 2000032990-A 1 02-FEB-2000;
COMMENT	SMITHKLINE BEECHAM CORP OS Unidentified PN JP 2000032990-A/1 PD 02-FEB-2000 PF 14-MAY-1999 JP 1999134172 PR 28-JAN-1997 US 08/790032 PI PETER R YOUNG PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,C07K14/545,C07K16/24, C12P21/02, PC C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53//A61K31/00,PC A61K31/00 PC A61K31/00,A61K31/00,C12N15/00,A61K37/02 CC Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers FT Source 1..1183 /organism='Unidentified'.
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Db 128	AATGTGTAACCATATTACTGGGACTATTATGATTTGAATCAGCAAGTGTGACCGCTTCA 187
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Db 188	GGGCAGAACCTTGTCGCCAGTTCACGAACTGACAGTGTGACCCAGTCACATTGCTGT 247
QY 138	aatctcatcgacagatgtggagacccttgagaagcacagagggaaacccatctacctgg 197 
Db 248	TATCATGTCAAGATATCCAGAGGCTCTTGAGCAAGCACAGAGGGATPCCAATTTATTGG 307
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Db 308	AATCCAGAATCCAGAAATGTTGTTGTTATGTGAGAGGTTGGAGAACACGCCACATTGCA 367
QY 258	gctgaagaaaaaggatataataggatttgtacaaccaaacccagacctgtgaagtctttct 317 
Db 368	GCTAAANGAGCAGAGATCATGTGATCTGTATGGCAAACCGAGCCGGTAAAACCTTCT 427
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Db 428	TTTCTACCTGCGCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCAGACTG 487
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Db 488	GTTCAT---TGCTCTCTCCAGAGAGACACAGCCCATCATTTCTGACTTCAGAACTTGGGAA 544
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RESULT 10	
AF200492	
LOCUS	AF200492 1183 bp mRNA linear PRI 11-MAY-2000
DEFINITION	Homo sapiens interleukin-1 homolog 1 mRNA, complete cds.

ACCESSION	AX052581	GI:12226796	
VERSION	AX052581.1		
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 585)		
TITLE	Sims, J.E. and Renshaw, B.R.		
JOURNAL	II-1 eta dna and polypeptides		
	Patent: WO 0071720-A 1 30-NOV-2000;		
	IMMUNEX CORPORATION (US)		
FEATURES	Location/Qualifiers		
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CDS	112..585		
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Qy	43 attcaggatataatcatcggtgtggtgtcttcaggaccagcgctcatagcagtcgcg 102		
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Qy	103 aggaagacccgtatgtctccagtcactatgtccttaatctcatgcgcacatgtggagacc 162		
Db	211 CTTAGCGCGAGCATTTAAGCCCTGTCTCTTCATTTAATAGCCCTGTAGAGACACAGAATTC 270		
Qy	163 ctgagaaagacagaggaaacccactctactctggcgtgaatgactcaatctctgcctg 222		
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Qy	403 ggctgcctctcatccttaccacaagaactgggaaagacaaacactactgaacttgggtta 462		
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RESULT	13		
AF201833			
LOCUS	AF201833	585 bp	mrna linear PRI 16-JAN-2000
DEFINITION	Homo sapiens FILL eta mRNA, complete cds.		
ACCESSION	AF201833		
VERSION	AF201833.1	GI:6694393	
KEYWORDS	human.		



SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 746)  
AUTHORS Busfield,S.J.  
TITLE Spoil-1 protein and nucleic acid molecules and uses therefor  
JOURNAL Patent: US 6197551-A 1 06-MAR-2001;  
FEATURES Location/Qualifiers  
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BASE COUNT 275 a 150 c 142 g 179 t  
ORIGIN

Query Match 27.1%; Score 129.2; DB 6; Length 746;  
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Job time: 15419 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 12:02:58 ; Search time 338.08 Seconds  
(without alignments)  
2422.409 Million cell updates/sec

Title: US-09-763-498-12  
Perfect score: 477  
Sequence: 1 atggaaaagcattgaaat.....ggttacatctgtgttttaa 477

Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_032802.\*  
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	477	21	AAZ51248
2	475.4	99.7	477	21	AAZ51247
3	462.8	97.0	819	22	AAZ51247
4	349.8	73.3	391	22	AAZ51247
5	238.6	50.0	809	19	AAZ51247
6	238.6	50.0	838	20	AAZ51247
7	213	44.7	213	21	AAZ51246
8	202	42.3	1073	22	AAZ512296
9	202	42.3	1183	19	AAZ512659

10	202	42.3	1183	20	AAZ51248	Human interleukin-1
11	202	42.3	1183	22	AAZ51248	Human cDNA encoding
12	202	42.3	1291	20	AAZ51248	cDNA encoding a hu
13	201.6	42.3	673	22	AAZ51248	Human cDNA encoding
14	201.6	42.3	673	22	AAZ51248	Human novel protei
15	201.4	42.2	1377	20	AAZ51248	cDNA encoding a hu
16	161.4	33.8	1321	21	AAZ51248	cDNA encoding a hu
17	161.4	33.8	1321	21	AAZ51248	cDNA encoding a hu
18	134.2	28.1	520	22	AAZ51248	Human IL-1 recepto
19	134.2	28.1	585	22	AAZ51248	Human interleukin-
20	134.2	28.1	1244	22	AAZ51248	Human IL-1 eta cDN
21	129.2	27.1	746	20	AAZ51248	Human interleukin-
22	127	26.6	219	19	AAZ51248	cDNA encoding a mu
23	86.6	16.2	174	21	AAZ51248	Rodent interleukin
24	74.8	16.5	1710	20	AAZ51248	Mouse interleukin-
25	74.8	15.7	1877	21	AAZ51248	Nucleotide sequenc
26	72.6	15.2	654	21	AAZ51248	Mouse interleukin-
27	71.8	15.1	531	22	AAZ51248	Human zilla4 degen
28	71.8	15.1	531	22	AAZ51248	Nucleotide sequenc
29	71.8	15.1	1577	19	AAZ51248	Nucleotide sequenc
30	71.8	15.1	1614	22	AAZ51248	Equine interleukin
31	71	14.9	654	21	AAZ51248	Nucleotide sequenc
32	70.8	14.8	456	14	AAZ51248	Human zilla4-E200K
33	70.8	14.8	462	18	AAZ51248	IL-1 inhibitor (IL
34	70.8	14.8	462	19	AAZ51248	Recombinant human
35	70.8	14.8	462	19	AAZ51248	Human interleukin-
36	70.8	14.8	514	16	AAZ51248	Human interleukin-
37	70.8	14.8	514	18	AAZ51248	Plasmid 15424. Sy
38	70.8	14.8	514	20	AAZ51248	DNA encoding leade
39	70.8	14.8	531	17	AAZ51248	Leaderless IL-1 re
40	70.8	14.8	531	17	AAZ51248	Human interleukin-
41	70.8	14.8	531	17	AAZ51248	Interleukin-1 rece
42	70.8	14.8	531	17	AAZ51248	Interleukin-1 rece
43	70.8	14.8	531	17	AAZ51248	Interleukin-1 rece
44	70.8	14.8	532	12	AAZ51248	IRAP gene. Homo s
45	70.8	14.8	540	10	AAZ51248	Sequence of bps 61

## ALIGNMENTS

RESULT 1	
AAZ51248	
ID AAZ51248 standard; DNA; 477 BP.	
XX AAZ51248;	
AC AAZ51248;	
XX AAZ51248;	
DT 06-JUN-2000 (first entry)	
XX Polymorphic human Interleukin-1 epsilon DNA.	
DE Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;	
XX immunosuppressant; antiarthritis; antiproliferative; antiproliferative;	
XX gene mapping; immune system; treatment; inflammatory disease;	
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;	
KW psoriasis; human; ds.	
XX Homo sapiens.	
OS Homo sapiens.	
FH Key	Location/Qualifiers
FT CDS	1..477
FT	/*tag= a
FT	/product= "Interleukin-1 epsilon polymorphic variant"
FT	/note= "Homologous to mouse IL-1 epsilon protein"
FT	replace (35, A)
FT	/*tag= b
FT variation	
PN WO200011174-A1.	
XX	
PD 02-MAR-2000.	
XX	
PF 20-AUG-1999;	99WO-US18771.
XX	



QY 241 gaccagccacactgcagctgaaggaaagatatataatgattgtacaaaccccgag 300  
 Db 241 gaccagccacactgcagctgaaggaaagatatataatgattgtacaaaccccgag 300  
 QY 301 cctgtgaagtccttctcttaccacagccagagtgccaggaactccaccttcagttc 360  
 Db 301 cctgtgaagtccttctcttaccacagccagagtgccaggaactccaccttcagttc 360  
 QY 361 gtgcttccctggctgttcagctgtcagctctgaaggaggtgctctctatcctt 420  
 Db 361 gtgcttccctggctgttcagctgtcagctctgaaggaggtgctctctatcctt 420  
 QY 421 acccaagaactgggaaagccaaactactgactttgggttaactatgctgttttaa 477  
 Db 421 acccaagaactgggaaagccaaactactgactttgggttaactatgctgttttaa 477

## RESULT 3

AA06911  
 ID AAD06911 standard; cDNA; 819 BP.

XX

AC AAD06911;

XX 03-AUG-2001 (first entry)

XX Human interleukin-1 receptor antagonist-like (IL-lra-L) cDNA.

XX Human: interleukin-1 receptor antagonist-like protein; IL-lra-L; therapy;  
 KW rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;  
 KW joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;  
 KW transplant rejection; graft versus host disease; strain; sprain; leprosy;  
 KW cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;  
 KW clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;  
 KW myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;  
 KW acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;  
 KW eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;  
 KW hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;  
 KW infertility; endometriosis; retinal neuropathy; acute pancreatitis;  
 KW Kawasaki's disease; cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..819

XX /\*tag= a

XX /product= "Human interleukin-1 receptor antagonist-like

XX (IL-lra-L) protein"

XX /note= "CDS does not include stop codon"

XX /partial

XX WO200141792-A1.

XX PN

XX PD

XX 14-JUN-2001.

XX 04-DEC-2000; 2000WO-US32891.

XX 10-DEC-1999; 99US-0170105.

XX 28-NOV-2000; 2000US-0724859.

XX (AMGE-) AMGEN INC.

XX Calzone FJ, Luethy R, Boedigheimer MJ, Zhu J, Chung Y, Jing S;  
 XX WPI; 2001-381495/40.

XX P-PSDB; AAE03417.

XX

XX Novel Interleukin-1 Receptor Antagonist-like nucleic acid molecule, the

XX polypeptide encoded by the nucleic acid is useful diagnosis, treatment,

XX and prevention of diseases such as arthritis, diabetes, transplant

XX rejection

XX

XX Claim 1; Fig 1A; 127pp; English.

XX

XX The present sequence is human interleukin-1 receptor antagonist-like  
 CC (IL-lra-L) cDNA. IL-lra-L is useful for treating, preventing or  
 CC ameliorating IL-lra-L polypeptide-related disease, condition or disorder  
 CC which include rheumatoid arthritis, psoriatic arthritis, inflammatory  
 CC arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,  
 CC lupus, diabetes, transplant rejection, inflammatory joint disease, graft  
 CC versus host disease and inflammatory conditions resulting from strain,  
 CC sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human  
 CC immunodeficiency virus (HIV) infection, clostridium-associated  
 CC diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,  
 CC anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory  
 CC disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,  
 CC psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,  
 CC Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,  
 CC lymphomas, lung and breast cancer, leukaemia, infertility,  
 CC endometriosis, retinal degeneration, retinal neuropathy, acute  
 CC pancreatitis and Kawasaki's disease.  
 XX  
 XX Sequence 819 BP; 202 A; 196 C; 204 G; 217 T; 0 other;

Query Match 97.0%; Score 462.8; DB 22; Length 819;

Best Local Similarity 99.6%; Pred. No. 6.4e-133;

Matches 464; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 agcattgaaattgacacactcagcggggagcattcaggatcatcaatcgcggtgtg 68

Db 354 aacattgaaattgacacactcagcggggagcattcaggatcatcaatcgcggtgtg 413

QY 69 ggttcctcaggacagcgtctatagcgtcccgaggagaccgtatgtctccagtcac 128

Db 414 ggttcctcaggacagcgtctatagcgtcccgaggagaccgtatgtctccagtcac 473

QY 129 tattgccttaattcattgcgcagcatgtggagacccttgagaaagacagaggaaccccat 188

Db 474 tattgccttaattcattgcgcagcatgtggagacccttgagaaagacagaggaaccccat 533

QY 189 ctacctgggctgaatggactcaatctctgcctgcgtgtgtgtctaaagtgcgggaccagcc 248

Db 534 ctacctgggctgaatggactcaatctctgcctgcgtgtgtgtctaaagtgcgggaccagcc 593

QY 249 cacactgcagctgaaggaaagatatataatggattgtacaacacccgacctgtgaa 308

Db 594 cacactgcagctgaaggaaagatatataatggattgtacaacacccgacctgtgtgaa 653

QY 309 gtctttctctcttaccacagccagagtgccaggaactccaccttcgactgtgtgtgtgt 368

Db 654 gtctttctctcttaccacagccagagtgccaggaactccaccttcgactgtgtgtgtgt 713

QY 369 ccttggtgtgtctcagctgtcagctgaaggaggtgtctctctatctaccacaga 428

Db 714 ccttggtgtgtctcagctgtcagctgaaggaggtgtctctctatctaccacaga 773

QY 429 actgggaaagccaaactactgactttgggttaactatgtgttt 474

Db 774 actgggaaagccaaactactgactttgggttaactatgtgttt 819

## RESULT 4

AA06911

ID AAF83870 standard; cDNA; 391 BP.

XX

AC AAF83870;

XX 06-AUG-2001 (first entry)

XX Human interleukin-1 receptor antagonist (NOVINTRA C) encoding cDNA.

XX NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;

XX gonadotropin-like protein; NOVGN; interleukin-1; NOVINTRA; human;

XX cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;

XX antibacterial; cerebroprotective; antidiabetic; antiarthritic;

XX

Db 115 aaagacagagggaaccccatctacctgggacctgaatggactcaatctctgcctgatgtgt 174

This cDNA encodes a rodent interleukin (IL)-1 epsilon polypeptide. The invention relates to a recombinant polypeptide that specifically binds polyclonal antibodies (Abs) generated against a 12 consecutive amino acid segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these IL polypeptides are used to regulate a cell involved in an inflammatory response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and the corresponding nucleic acids regulate development and/or the immune system, and can be used to diagnose and treat conditions associated with abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1 epsilon polypeptides are used with agonists or antagonists of IL-1 alpha, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1 epsilon polypeptides may be used as a soluble polypeptide or as a fusion protein.

CC protein with another cytokine or chemokine.

XX Sequence 809 BP; 241 A; 180 C; 179 G; 209 T; 0 other;

SQ

Query Match 50.0%; Score 238.6; DB 19; Length 809;  
Best Local Similarity 68.8%; Pred. No. 1.3e-63;  
Matches 328; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

YY 1 atggaagaagcattgaaatggacacacctgcaggcggggagcttcaggatatcaatcat 60  
Db | ||| |||| || | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 96 aaggagaagaactaagcagcagcatccctcgttagacatggtcaggatcttagtct 155  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 61 cgggtgtgggtttcaccagcagcagcgtcctatagcagcagcagcagcagcagcagc 120  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 156 cgtgtgtgatcctgcagacaatactcctcactcagtcaccaaggaaagcacaagt 215  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 121 caagtcaactatgcttaattctatcgcgcacatgctggagacccttgagaaaagacag 180  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 216 caagtcaactatcactgtcctccatgccaatctggcacactcttgagacgaacagg 275  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 181 aaccacatctcctggcctgaatgactgaactctcgtcgtgctgtgctaaagtcgg 240  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 276 gatcccacgtacatgggagtgcaaagccgagcgtgctgttgcacaaagatggg 335  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 241 gaccagccaactcagctgaaagaaaagataatgatttgttacaccaaccagg 300  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 336 gagcagctctgtctacagcttgggaagggaacataatggaatgtacacaaaaaggaa 395  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 301 cctgtgaagctctctctcttaccacagcagagtgccaggaactccaccttcagct 360  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 396 cctgtaaaagcctctctcttatcacaagaagtgtagaacacctctacattgagct 455  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 361 gtgcttccccgtgtgttactcgtctgaactctgaaaggagctgtctctctcatt 420  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 456 gcagcctccctcgtgtgttcacgtctgtctgtcttaaaggagctgccaactcatt 515  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 421 acccaagaactgggaagacacacactactgacttgggttaactatgctgttttaa 477  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |  
YY 516 acccaagaactgggaagacacacactactgacttgggttaactatgctgttttaa 572  
Db | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | | |||| | |

RESULT 6

AA86460 standard; cDNA; 838 BP.

ID AAX86460;

XX AAX86460;

DT 30-SEP-1999 (first entry)

DE cDNA encoding a murine SPOIL-II protein.

XX SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent; bone metabolism disorder; proinflammatory disorder; immune disorder; inflammatory disease; septic shock; stroke; diabetes; arthritis; intercolitis; pneumonitis; epithelial cell; skin disease; proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma; epithelial cancer; squamous cell carcinoma; bone resorption disorder; osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis; osteogenesis imperfecta; fibrous dysplasia; hypophosphatasia; bone sarcoma; myeloma bone disorder; osteolytic bone lesion; hypercalcaemia; bone mass; bone fragility; bone pain; bone deformity; bone fracture; ss.

XX Mus sp.

OS

XX Key

FH Location/Qualifiers

FT 96..578

FT /\*tag= a

FT /product= SPOIL-II

XX W09037662-Al.

PX

Db 462 gcagcttcctcgttggttcacgtctgctctctaaaggagctgccactcattctg 521  
 Qy 421 accaagaactggggaagaaacacactactgacttgggttaactatgctgttttaa 477  
 Db 522 accaagaactggggaagaaactcttcactcactgacttcgagatgattgggtacattaa 578  
 RESULT 7  
 AAZ51246  
 ID AAZ51246 standard; DNA; 213 BP.  
 XX AAZ51246;  
 XX 06-JUN-2000 (first entry)  
 XX 3' exon of human Interleukin-1 epsilon DNA.  
 XX Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
 KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;  
 KW gene mapping; immune system; treatment; inflammatory disease;  
 KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
 KW psoriasis; human; ds.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 CDS 1..213  
 FT /\*tag- a  
 FT /partial  
 FT /product= "Partial human IL-1 epsilon protein"  
 FT /note= "Homologous to mouse IL-1 epsilon protein"  
 XX WO200011174-A1.  
 XX  
 XX PD 02-MAR-2000.  
 XX PF 20-AUG-1999; 99WO-US18771.  
 XX PR 21-AUG-1998; 98US-0097413.  
 XX PR 31-AUG-1998; 98US-0098595.  
 XX PR 11-SEP-1998; 98US-0099974.  
 XX PA (IMV ) IMMUNEX CORP.  
 XX Sims JE, Smith DE;  
 XX WPI; 2000-237653/20.  
 XX P-PSDB; AAY70216.  
 XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
 PT treat inflammatory and immune system-related diseases such as  
 PT rheumatoid arthritis and inflammatory bowel disease -  
 XX Claim la; Fig 1; 76pp; English.  
 XX The present sequence is the 3' exon of human Interleukin-1 (IL-1)  
 CC epsilon DNA. IL-1 epsilon gene is mapped to chromosome 2q and is mainly  
 CC expressed in spleen; lymph node, thymus, tonsil and leucocyte tissues.  
 CC IL-1 epsilon is a cytokine, with antiinflammatory, immunosuppressant,  
 CC antirheumatic, antiarthritic and antipsoriatic activity. The DNA  
 CC sequence can be used in chromosome identification, gene mapping and  
 CC study of immune system. IL-1 epsilon can be used in the treatment of  
 CC inflammatory or autoimmune diseases such as rheumatoid arthritis,  
 CC inflammatory bowel disease and psoriasis.  
 XX Sequence 213 BP; 51 A; 56 C; 48 G; 58 T; 0 other;  
 SQ  
 Query Match 44.7%; Score 213; DB 21; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 6e-56;  
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 265 gaaagagataatgattgtacacacacccgagcctgtgaagctctcttcttctac 324

Db 1 gaaagagataatgattgtacacacacccgagcctgtgaagctctcttcttctac 60  
 Qy 325 cacagccagagtgccaggaactccacttcgagtgctgtggtttccctggctggttcac 384  
 Db 61 cacagccagagtgccaggaactccacttcgagtgctgtggtttccctggctggttcac 120  
 Qy 385 gctgcagctctgaaggagcgtctctctcctcctaccacgaactggggaagcacaac 444  
 Db 121 gctgcagctctgaaggagcgtctctcctcctcctaccacgaactggggaagcacaac 180  
 Qy 445 actactgacttgggttaactatgctgttttaa 477  
 Db 181 actactgacttgggttaactatgctgttttaa 213  
 RESULT 8  
 RAD12296  
 ID RAD12296 standard; DNA; 1073 BP.  
 XX AAD12296;  
 XX 16-OCT-2001 (first entry)  
 XX Human interleukin-lepsilon (IL-lepsilon) protein DNA.  
 XX Human; interleukin-lepsilon; IL-lepsilon; virucide; hepatotropic; fever;  
 KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;  
 KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;  
 KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening; ds.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 CDS 67..576  
 FT /\*tag- a  
 FT /product= "Human interleukin-lepsilon (IL-lepsilon)  
 FT protein"  
 XX WO200157219-A2.  
 XX 09-AUG-2001.  
 XX PF 01-FEB-2001; 2001WO-US03285.  
 XX PR 02-FEB-2000; 2000US-0179638.  
 XX PA (SCHE ) SCHERING CORP.  
 XX Debets JEMA, Timans JC, Bazan JF, Kastelein RA;  
 XX WPI; 2001-48886/53.  
 XX P-PSDB; AAE06656.  
 XX Novel isolated or recombinant antigenic interleukin-1 delta or epsilon  
 PT polypeptide useful for treating conditions exhibiting abnormal  
 PT expression of interleukin such as immunological disorders, tumor and  
 PT allergy -  
 XX Claim 18; Page 86-87; 103pp; English.  
 XX The invention relates to recombinant antigenic interleukin-1 like  
 CC molecules and their corresponding nucleic acid sequences, designated  
 CC as interleukin-1delta (IL-1delta) and interleukin-lepsilon (IL-lepsilon).  
 CC IL-1delta and IL-lepsilon are useful for treating conditions exhibiting  
 CC abnormal expression of the interleukin such as immunological disorders,  
 CC tumours, inflammatory diseases, fever, hypoglycaemia, psoriasis,  
 CC allergy, autoimmune diseases and infectious diseases (e.g. pulmonary  
 CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as  
 CC HIV). The invention also relates to methods of using the composition  
 CC containing IL-1delta or IL-lepsilon for both diagnostic and therapeutic  
 CC utilities. IL-1delta is used as an immunogen for the production of  
 CC antisera or antibodies specific, e.g., capable of distinguishing between



Db 545 gtcatacaactgcttgaattaaat 574

RESULT 10

AAX90135  
ID AAX90135 standard; cDNA; 1183 BP.

XX AC AAX90135;

XX DT 20-SEP-1999 (first entry)

XX DE Human interleukin-1 receptor antagonist beta encoding cDNA.

XX KW Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicaemia;

XX KW Chronic inflammation; acute inflammation; arthritis; autoimmunity;

XX KW Inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;

XX KW Cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;

XX KW Traumatic brain injury; AIDS; cachexia; allergy; parasite infection;

XX KW Allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;

XX KW Allergic inflammatory disease; delayed hypersensitivity; vaccine; ss.

XX OS Homo sapiens.

XX PN W09936541-A1.

XX PD 22-JUL-1999.

XX PF 14-JAN-1999; 99WO-US00847.

XX PR 29-APR-1998; 98US-0069619.

XX PR 14-JAN-1998; 98US-0007464.

XX PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX PI Marshall L, Young PR;

XX DR WPI; 1999-430615/36.

XX DR P-PSDB; AAY24395.

XX PT New interleukin-1 receptor antagonist beta, useful for treating

XX PT Inflammation and autoimmune diseases

XX PS Claim 5; Fig 1; 34pp; English.

XX CC The present sequence encodes human interleukin-1 receptor antagonist

XX CC beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are

XX CC useful for diagnosing diseases (or susceptibility to diseases) related

XX CC to the expression or activity of IL-1RA beta, by determining mutations

XX CC in the IL-1RA beta nucleic acid sequences and/or analysing for the

XX CC presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides

XX CC are also useful for screening for compounds which affect activity of the

XX CC protein. These can be used in treatment to inhibit (antagonist) or

XX CC enhance (agonist) IL-1RA beta activity, in addition to direct

XX CC administration of IL-1RA beta polypeptides to treat conditions, or

XX CC direct administration of antisense sequences to prevent expression.

XX CC IL-1RA beta polypeptides (administered directly, in a vector i.e. gene

XX CC therapy, and as a vaccine) and antibodies induce an immune response to

XX CC immunise and prevent disease. Diseases diagnosed, prevented or treated

XX CC include chronic and acute inflammation, septicemia, arthritis,

XX CC inflammatory bowel disease, graft vs. host disease, autoimmunity,

XX CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),

XX CC psoriasis, restenosis, traumatic brain injury, AIDS, cachexia, allergy,

XX CC parasite infection, allergic rhinitis, allergic asthma, atopic

XX CC dermatitis, allergic inflammatory diseases and delayed hypersensitivity.

XX SQ Sequence 1183 BP; 329 A; 249 C; 269 G; 336 T; 0 other;

Query Match 42.3%; Score 202; DB 20; Length 1183;  
Best Local Similarity 67.1%; Pred. No. 3.3e-52;  
Matches 302; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

QY 18 aattgacacacacgcgagcgaggagcattcaggatataatcatcggtgtggtttctca 77  
Db 128 aatgtgtaaacctattactgggaactattaatgattgaatcagcaagtgtggaccctca 187  
QY 78 ggaccagagcgtctctcagcagtcgagagaccgtatgtctcagtcactattgctt 137  
Db 188 gggtcagaaacctgtggcagttccacgaagtgcagtggtgaccccgatcactgtgtgt 247  
QY 138 aatctcatgcccgcacatgtggagacccttgagaagacagagaggggaaccccatctacctggg 197  
Db 248 tatcacatgcaagtattccagagcctcttgagcaaggcagagggatccattttattggg 307  
QY 198 cctgtaatggactcaatctctcgtcgtgatgtgctaaagtcggggaccagccacactgca 257  
Db 308 aatccagaaatccagaaatgtgtgtattgtgagaaggttgagaaacagaccacattgca 367  
QY 258 gctgaagaaaaggataaataagattgtacacacacccagcctgtgaagtccttct 317  
Db 368 gtaaaagagcagaagatcattgattgtatggcaacccgagccctggaaccccttct 427  
QY 318 cttctaccacagccagagtgagcaggaactccacactctgagtcgtgtgcttccctggctg 377  
Db 428 ttctaccgtgcgaagactgtgagacctccacctgagtcgtgcttccctggctg 487  
QY 378 gttcatcgctgtcagctctgaaggagcgtgtcctctcatccttaccacaaactgggaa 437  
Db 488 gtccat---tgctctccaaagagagaccagccacattctgactcagaacttgggaa 544  
QY 438 agccaacactactgacttgggttaactat 467  
Db 545 gtcatacaactgcttgaattaaat 574

RESULT 11

AAS26842  
ID AAS26842 standard; cDNA; 1183 BP.

XX AC AAS26842;

XX DT 07-NOV-2001 (first entry)

XX DE Human cDNA encoding a novel secreted protein, SEQ ID 34.

XX KW Human; immunosuppressive; antiarthritic; ss; antirheumatic;

XX KW cytostatic; cardiant; vasotropic; cerebroprotective; neurotropic;

XX KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;

XX KW vulnary; secreted protein; rheumatoid arthritis;

XX KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;

XX KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;

XX KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;

XX KW corneal infection; wound healing; epithelial cell proliferation;

XX KW skin ageing; food additive; preservative; antiproliferative.

XX OS Homo sapiens.

XX PN WO200155441-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01320.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.  
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PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
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PR 14-AUG-2000; 2000US-0224518.  
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PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
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PR 29-SEP-2000; 2000US-0236368.  
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PR 29-SEP-2000; 2000US-0236370.  
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PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
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PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.

PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
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PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
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PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
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PR 17-NOV-2000; 2000US-0249244.  
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PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI: 2001-476222/51.  
XX P-PSDB; AAU16937.  
XX  
XX Novel polypeptides and polynucleotides useful as diagnostic reagents to  
XX diagnose diseases or disorders associated with aberrant expression or  
XX activity of polypeptides, for treating blood clotting disorder,  
XX haemophilia -  
PS Claim 1; SEQ ID No 34; 601pp; English.  
XX

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in

CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
 CC immunosorbent assays (ELISA). Disorders which are diagnosed or treated  
 CC include autoimmune diseases e.g. rheumatoid arthritis,  
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
 CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.  
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
 CC and ocular disorders e.g. corneal infection, and many other  
 CC disorders listed in the specification. The polypeptides can also  
 CC be used to aid wound healing and epithelial cell proliferation, to  
 CC prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
 CC as a food additive or preservative to increase or decrease storage  
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
 CC minerals, cofactors and other nutritional components. The present

Query Match 42.3%; Score 202; DB 22; Length 1183;  
 Best Local Similarity 67.1%; Pred. No. 3.3e-52;  
 Matches 302; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

QY 18 aattgacacacccagcggggagcattcaggatcataatcagcgggtgtgtgtttcttca 77  
 DB 128 aatgtgtaaacctattactggtgacttaattgattgaatcagcaagtgtggaccttca 187  
 QY 78 ggaccagacgtcatagcagctccggaggagcagcgtatgtctccagtcactattgctt 137  
 DB 188 gggtcagaacctgtgtgagctccacgaagtgcagctgtgaccccaagtcactgtgtgt 247  
 QY 138 aatctatgcgcagatgtggagacccttgagaaagacagagggaaccccatctacctggg 197  
 DB 248 tatcatgcaagtattccagagcgtcttgagcaaggcagagggatcccatattattggg 307  
 QY 198 cctgaatggactcaactctcgtcgtatgtgtgctaaagtgggagaccacacactgca 257  
 DB 308 aatccagaatccagaaatgtgtgtgtgtgagaaaggttggagacagccacactgca 367  
 QY 258 gctgaagagaaagataatgattgtatcaaccacccagcgtgtgaaagtcctttct 317  
 DB 368 gctaaagagacagaatcatgagctgtgtatgccaaccgacccgtgaaaccttct 427  
 QY 318 ctttaccagcagagtgaggcaggaaactccacctcgtatgtgtgttccctgctg 377  
 DB 428 ttttaccgtgccaagagctgtgagcctccaccccttgatgtgtgtgtcctccgactg 487  
 QY 378 gttcatcgtcgtcagctgaagagcgtctcctcactccttaccagaagactgggaa 437  
 DB 488 gttcat---tgctcctcccaagagagaccagcccatcactcgtcagaaactgggaa 544  
 QY 438 agccaacactactgacttgggttaactat 467  
 DB 545 gtcataacacactgcttgaattaatat 574

RESULT 12  
 AAX86458  
 ID AAX86458 standard; DNA: 1291 BP.  
 XX  
 AC AAX86458;  
 XX  
 DT 30-SEP-1999 (first entry)  
 XX  
 DE cDNA encoding a human SPOIL-I protein (also known as hTANGO 080-I).  
 XX  
 KW SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;  
 KW bone metabolism disorder; proinflammatory disorder; immune disorder;  
 KW inflammatory disease; septic shock; stroke; diabetes; arthritis;  
 KW intercolitis; pneumonitis; epithelial cell; skin disease;  
 KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;  
 KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;  
 KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;  
 KW osteogenesis imperfecta; fibrous dysplasia; hypophosphatasia;  
 KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;

KW hypercalcaemia; bone mass; bone fragility; bone pain; bone deformity;  
 KW bone fracture; hTANGO 80-I; ss.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 CDS 124..633  
 FT /\*tag= a  
 FT /product= SPOIL-1  
 XX  
 FT  
 PN W09937662-A1.  
 XX 29-JUL-1999.  
 PD  
 XX 26-JAN-1999; 99WO-US01575.  
 PF  
 XX 27-JAN-1998; 98US-0013810.  
 PR  
 XX (MILL-) MILLENNIUM BIOPHARMACEUTICS INC.  
 PA  
 XX Busfield SJ;  
 PI  
 XX WPI: 1999-458675/38.  
 DR P-PSDB: AAY24043.  
 XX  
 XX New isolated SPOIL proteins, used to develop products for treating,  
 PT e.g. inflammatory and immune disorders  
 PT  
 XX Example 1; Fig 4A-B; 126pp; English.  
 PS

XX The present sequence encodes a SPOIL-I protein. The SPOIL proteins have  
 CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.  
 CC The SPOIL proteins are used as modulating agents in regulating a variety  
 CC of cellular processes. The products can be used for treating disorders  
 CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone  
 CC metabolism disorder, a proinflammatory disorder or an immune disorder.  
 CC They can be used for treating e.g. inflammatory diseases and disorders  
 CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,  
 CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and  
 CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma  
 CC and Kaposi's sarcoma and other epithelial cancers including squamous cell  
 CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and  
 CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's  
 CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,  
 CC fibrous dysplasia, hypophosphatasia, bone sarcoma, myeloma bone disorder  
 CC (e.g. osteolytic bone lesions) and hypercalcaemia. SPOIL molecules and  
 CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in  
 CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.  
 CC decrease bone fragility); and prevention and/or treatment of bone pain,  
 CC bone deformities and/or bone fractures. The products can also be used for  
 CC detection, diagnosis and screening assays.

XX Sequence 1291 BP; 375 A; 271 C; 291 G; 354 T; 0 other;

Query Match 42.3%; Score 202; DB 20; Length 1291;  
 Best Local Similarity 67.1%; Pred. No. 3.4e-52;  
 Matches 302; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

QY 18 aattgacacacccagcggggagcattcaggatcataatcagcgggtgtgtgtttcttca 77  
 DB 177 aatgtgtaaacctattactggtgacttaattgattgaatcagcaagtgtggaccttca 236  
 QY 78 ggaccagacgtcatagcagctccggaggagcagcgtatgtctccagtcactattgctt 137  
 DB 237 gggtcagaacctgtgtgagctccacgaagtgcagctgtgaccccaagtcactgtgtgt 296  
 QY 138 aatctcatcgcagatgtgtgagaccccttgagaaagacagagggaaccccatcactctggg 197  
 DB 297 tatcatgcaagtattccagagcgtcttgagcaaggcaggggtatcccatattattggg 356  
 QY 198 cctgaatgactcaactctcgtcgtatgtgtgctaaagtgggagccacacactgca 257

Db 357 aatccagaatccagaaatgtgtttgtattgtgagaaggttgagaacagccacacattgca 416  
Qy 258 gctgaagaaaagataaagtattgttacaaacccgagcctgtgaagtcctttct 317  
Db 417 gctaaaagacagaagatgatgtatgtgccaacccgagcccgtaaaccttctct 476  
Qy 318 cttctaccacagcagagtgagcgaactccacttcgagctgtggtttccctggctg 377  
Db 477 ttctaccgtgccagactgtaggacctccaccttgatgtgtggtcctcccgactg 536  
Qy 378 gttcatcgctcagctctgaagagcgtgctctctccttaccacaaagactgggaa 437  
Db 537 gttcat---tgcctcctccaagagaccagcagcccatcattctgacttcgaactgggaa 593  
Qy 438 agccaacactactgactttgggttaactat 467  
Db 594 gtcatacacactgcctttgaataatat 623  
  
RESULT 13  
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ID AAS26915 standard; cDNA; 673 BP.  
XX XX  
AC AAS26915;  
XX XX  
DT 07-NOV-2001 (first entry)  
XX XX  
DE Human cDNA encoding a novel secreted protein, SEQ ID 107.  
XX XX  
KW Human; immunosuppressive; antiarthritic; ss; antirheumatic;  
KW cytosolic; cardiant; vasotropic; cerebroprotective; nootropic;  
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
KW vulary; secreted protein; rheumatoid arthritis;  
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
KW corneal infection; wound healing; epithelial cell proliferation;  
KW skin ageing; food additive; preservative; antiproliferative.  
OS Homo sapiens.  
XX XX  
PN WO20015441-A2.  
XX XX  
PD 02-AUG-2001.  
XX XX  
PF 17-JAN-2001; 2001WO-US01320.  
XX XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180828.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
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PR 14-AUG-2000; 2000US-0224519.  
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PR 22-AUG-2000; 2000US-0226681.  
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PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
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PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
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PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
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PR 14-SEP-2000; 2000US-0233064.  
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PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
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PR 02-OCT-2000; 2000US-0236802.  
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PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.





KW bone metabolism disorder; proinflammatory disorder; immune disorder;

335 aaccttatggcagattccacgaaatgacagatgtgaccccaatcactatttgcctattatcaca 394





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 11:09:01 ; Search time 2828.95 Seconds  
(without alignments)  
2275.773 Million cell updates/sec

Title: US-09-763-498-12  
Perfect score: 477  
Sequence: 1 atggaaaaagcatgaaaaa.....ggttaactatctgttttaa 477

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	238.6	50.0	883	11 AK004061	AK004061 Mus muscu
2	129.2	27.1	479	9 AA030324	AA030324 mi08c10.i
C 3	124.4	26.1	612	10 BM386666	BM386666 UI-R-CN1-
C 4	122	25.6	539	9 AW368430	AW368430 CM3-HT019
5	122	25.6	555	9 AW368437	AW368437 CM3-HT019
C 6	122	25.6	557	9 AW368437	AW368437 CM3-HT019
C 7	122	25.6	559	9 AW578451	AW578451 RCI-CT025
C 8	121	25.4	555	10 BE695960	BE695960 RCI-CT025
C 9	120.4	25.2	436	9 AW361164	AW361164 RCI-CT025
10	120.4	25.2	536	9 AW853610	AW853610 RCI-CT025
11	120	25.2	1219	11 AK009787	AK009787 Mus muscu
12	113.2	23.7	870	10 BF244205	BF244205 601863146
C 13	111	23.3	434	9 AW753217	AW753217 RCI-CT025
14	97.4	20.4	560	9 AW361245	AW361245 RCI-CT025
15	74.8	15.7	1020	10 BG245180	BG245180 602357579
16	72	15.1	997	9 AL554778	AL554778 AL554778
17	71.8	15.1	594	10 BI961215	BI961215 MONO1_7_E

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19	71.4	15.0	435	10 W78043	W78043 zd72d01.r1
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24	70.8	14.8	955	10 BM009048	BM009048 603618892
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30	65	13.6	531	9 AW951593	AW951593 EST363663
31	62.6	13.1	393	9 AV011778	AV011778 AV011778
32	62	13.0	832	10 BI517352	BI517352 603041588
33	61.4	12.9	900	11 AY026753	AY026753 Homo sapi
C 34	61.2	12.8	350	10 BI020732	BI020732 CM4-WT021
35	61.2	12.8	1051	11 AK009741	AK009741 Mus muscu
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37	60.8	12.7	726	10 BI089828	BI089828 602855071
38	60.8	12.7	858	10 BI090567	BI090567 602855674
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40	60.4	12.7	726	10 BI766516	BI766516 603052319
41	56.8	11.9	824	10 BI762103	BI762103 603049281
42	56.2	11.8	690	10 BI912302	BI912302 603069864
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ALIGNMENTS

RESULT 1

AK004061

LOCUS

DEFINITION

AK004061

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

AK004061 883 bp mRNA linear HTC 19-JAN-2002  
Mus musculus 18 days embryo whole body cDNA, RIKEN full-length  
enriched library, clone:1110033G16: Interleukin 1 family, member 6  
(epsilon), full insert sequence.

AK004061 GI:12835089  
HTC; CAP trapper.  
Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA,  
clone\_lib:RIKEN full-length enriched mouse cDNA library  
clone:1110033G16.

Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (sites)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)

2 (sites)  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)

3 (sites)  
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,  
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakauchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M.,  
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,  
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

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Oy	61 cgggtggtggtttctcaggaccacacactcagcagctcccgaggaagaccgtatgtct 120				
Db	228 CGTGTGGATTCCTGCAGACAAATATCTCTACTCGATGCCAAGGAAGAGCAACAGATT 287				
Oy	121 ccagtccattgcttaattcctcgcgacatgagagaccccttgagaagacagagggg 180				
Db	288 CCAGTCACTATTACTTTCCTCCCATGCCAATATCTGGACACTCTTGAGACGACAGGGG 347				
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Oy	241 gaccagccacacgtgcagctgaagaaaagatataatggattgttacaacaccccgag 300				
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Db	528 GCAGCCTTCCCTGGTGTGTTTCATCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 587				
Oy	421 acccaagacgtgggaaagcccaactactgacttgggttgaactctgttttaa 477				
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AA030324 479 bp mRNA linear EST 21-JAN-1997  
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 DEFINITION clone IMAGE:459858 5', mRNA sequence.

ACCESSION AA030324  
 VERSION AA030324.1 GI:1497479  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 479)  
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
 TITLE The WashU-HHMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:276746  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 467.

20530913  
 11076861  
 4 (sites)  
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
 5 (bases 1 to 883)  
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Furukuni, Y., Furuno, M., Hanegaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCCGACCTCGAGTGTGTTTGTGTTT 3'], cDNA was prepared by using triazole thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGGATTCAGAGCTCAATTAATTAATTAACCCCTCCCTCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.  
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FEATURES
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1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TCTTACCATCTGAAGTGGAGCGCGGAAATTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 148 a 108 c 102 g 121 t
ORIGIN

Query Match 27.1%; Score 129.2; DB 9; Length 479;
Best Local Similarity 73.9%; Pred. No. 5.9e-28;
Matches 164; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Db 195 cagcttcagaaaggaacataatgaaatgctacacaaaggaacctgttaaagcctt 254
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QY 316 ctctttaccacagcagatgagcaggaacacaccttcagctgtgcttcctgcgc 375
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Db 255 CTCTTCTACACAGAGAGTGTACAACTCTACATTTGAGTCTGCAGCCTTCCTGGT 314
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 376 tggttcagctgtcagctgtgaagagagctgtcctctctaccccaagaactgggc 435
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Db 315 TGGTTTCATGCTGTGCTCTAAAGGAGCTGCCACTCATCTTGACCCCAAGACTGGG 374
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QY 436 aagcccaacactactgacttgggttaactatgctgttttaa 477
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RESULT 3
BM386666/c
LOCUS
DEFINITION
UI-R-CN1-cj9-l-09-0-UI.s1 UI-R-CN1 Rattus norvegicus cDNA clone
BM386666
BM386666
VERSION
BM386666.1 GI:18186719
KEYWORDS
EST.
SOURCE
Norway rat.
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 612)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the

```

oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized fundus library cDNA Library Preparation: M.B. Soares Lab Genetics (www.resgen.com) clones will be available through Research Seq primer: M13 Forward POLYA=Yes.

Location/Qualifiers  
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/clone\_lib="UI-R-CN1"  
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-CN1 library is a subtracted library derived from the following pool of seven normalized rat libraries: normalized rat seminal vesicles, normalized rat penis, normalized rat bladder, normalized rat cervix, normalized rat brown adipose, normalized rat fundus, and normalized rat salivary gland. It was constructed according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the CN1 library, plasmid DNA from the pool of normalized libraries was electroporated into competent bacteria for the production of single-stranded circular DNA. This was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template from the Rat Uenigene Set corresponding to plates R-5-AA-NN excluding plates R-5-MM and MN. This pool represented 40% of the final driver population. b) a pool of about 29,000 clones from subtracted libraries CA0 and CA1 corresponding to plates R-CA0-AWV through R-CA0-AXS, R-CA0-AZX through R-CA0-BAZ, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS, R-CA0-BKE, R-CA0-BKJ-K, R-CA0-BKJ-V, R-CA0-BKP through R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA, R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through R-CA0-BOD, R-CA0-BPA through R-CA0-BPF, R-CA0-BBA through R-CA1-BDA, R-CA1-BHZ through R-CA1-BJF, R-CA1-BJR, R-CA1-BJT through R-CA1-BKE, R-CA1-BLF, R-CA1-BKH, R-CA1-BKI, R-CA1-BKT, R-CA1-BL, R-CA1-BLH through R-CA1-BLN, R-CA1-BLS, R-CA1-BLU-V, R-CA1-BNR, and R-CA1-BLE. The resulting pool represented 20% of the final driver population. c) a pool of about 15,000 clones from non-normalized libraries CS0s, CT0s, CU0s, CW0s, CX0s and normalized libraries CS0, CT0, CU0, CW0, and CX0 corresponding to plates R-CS0s-CBD through R-CS0s-CBO, R-CT0s-CAM through R-CT0s-CAX, R-CU0s-CBP through R-CU0s-CCA, R-CW0s-CCB through R-CW0s-CCM, R-CX0s-CCN through R-CX0s-CCX, R-CS0-BSB, R-CS0-BTD through R-CS0-BTV, R-CS0-BVM, R-CT0-BTW through R-CT0-BUP, R-CT0-BVN, R-CW0-BUQ through R-CW0-BVL, R-CW0-BVW through R-CW0-BWP, R-CX0-BXN through R-CX0-BXO, R-CX0-BWQ through R-CX0-BXM. The resulting pool represented 5% of the final driver population. d) a pool of about 5,000 clones (1,000 from non-normalized eye library CV0 and 4,000 from normalized eye library CV1) corresponding to plates R-CV0-BRH through R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through R-CV1-BTC, and R-CV1-BVO through R-CV1-BVU. This pool represented about 5% of the final driver population. e) A pool of about 10,000 clones from subtracted library BS2, BV0 and BV0p (7-9.5 kb cDNA library fraction from rat whole embryo), and BX0 (0.5-7kb cDNA library fraction from rat whole embryo) corresponding to plates R-BS2-BDB through R-BS2-BFB, R-BV0-ANK through R-BV0-ANR, R-BV0p-AOI through R-BV0p-AOX, and R-BX0-AQY through R-BX0-ASH. The resulting pool represented 5% of the final driver

population. f) a pool of about 7,000 clones from the seven non-normalized libraries that make up the tracer including CV0, C20, DA0, DB0, DC0, DD0, and DE0 corresponding to plates R-CY0-BXP through R-CY0-BXZ, R-C20-BYA through R-C20-BYI, R-C20-B2B-C, R-DA0-BYJ through R-DA0-BYP, R-DA0-B2D through R-DA0-B2H, R-DB0-BYQ through R-DB0-BZA, R-DC0-B2I through R-DC0-B2Q, R-DD0-BYQ through R-DD0-B2A, R-DD0-B2R through R-DD0-B2C, R-DE0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The resulting pool represented about 10% of the final driver population. g) a pool of about 2,000 clones from the pool of normalized libraries, CN0, that makes up the tracer. The corresponding plates are R-CN0-BKX through R-CN0-BLD, R-CN0-BLG, R-CN0-BLP through R-CN0-BLR, R-CN0-BLT, R-CN0-BLW-X, R-CN0-BMB, and R-CN0-BMF through R-CN0-BML. This pool represented 5% of the final driver population. h) a pool of the 28 most abundant clones in the CN0 pool corresponding to the following addresses: bkx-a-09-0-UI, bkx-b-09-0-UI, bkx-b-11-0-UI, bkx-b-10-0-UI, bkx-d-01-0-UI, bkx-d-06-0-UI, bkx-g-08-0-UI, bkx-h-12-0-UI, bkx-a-05-0-UI, bkz-a-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI, bkz-c-09-0-UI, bkz-d-10-0-UI, bla-a-01-0-UI, bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI, blb-a-12-0-UI, blb-f-02-0-UI, blc-a-11-0-UI, blc-e-95-0-UI, bld-1-08-0-UI, bld-f-02-0-UI, blq-h-04-0-UI, blr-a-05-0-UI, blt-f-08-0-UI. This pool represented 5% of the final driver population. i) One abundant CN0 clone (corresponding to the address bkz-a-11-0-UI) was digested with Not I and Eco RI and the resulting insert was gel purified. This purified insert was added directly to the driver so that it represented 5% of the final driver population.

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TAG\_TISSUE=fundus  
TAG\_SEO=TTCCG

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Db	279	CCTCTCCACAGACAGACAAACATCAITCTTTACAGAGAGGGGTGAAGCTAATAACA	220		
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AW368430/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW368430  
CM3-HT0192-071099-022-e12 HT0192 Homo sapiens cDNA, mRNA sequence.  
AW368430  
AW368430.1 GI:6873080  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
HCGP <http://www.ludwig.org.br/ORESTES>.  
The FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
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BASE COUNT 145 a 131 c 123 g 140 t  
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RESULT 5  
AW361172

LOCUS AW3611172 555 bp mRNA linear EST 04-FEB-2000  
DEFINITION RCL1-CT0251-141099-012-h04 CT0251 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW3611172  
VERSION AW3611172.1 GI:6865822  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 555)  
AUTHORS HCGP <http://www.ludwig.org.br/OPRESTES>.  
TITLE The FAPESP/LICR Human Cancer Genome Project  
JOURNAL Unpublished (1999)  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
project. This entry can be seen in the following URL  
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Seq primer: puc 18 forward  
High quality sequence stop: 555.

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DEFINITION	CM3-HT0192-071099-022-h06 HT0192 Homo sapiens cDNA, mRNA sequence.	

ACCESSION	REFERENCE
VERSION	AUTHORS
KEYWORDS	TITLE
SOURCE	JOURNAL
ORGANISM	COMMENT

AW358437  
AW358437.1 GI:6873087  
EST.  
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Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 557)  
HCGP <http://www.ludwig.org.br/ORESTES>.  
The FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-Hr0192-071059-022-h06&t3=1995-10-07&t4=1>)  
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FEATURES	SOURCE
BASE COUNT	ORIGIN

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LOCUS  
DEFINITION  
ACCESSION

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RC1-CT0252-030100-023-b06 CT0252 Homo sapiens cDNA, mRNA sequence.  
AW578451

**KEYWORDS** EST.  
SOURCE Homo sapiens  
**ORGANISM** Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 555)  
**AUTHORS** Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.O., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,  
M.J., Soares,F., Brentani,R.K., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

**JOURNAL MEDLINE COMMENT**  
Contact: Simpson A J G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel.: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
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SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
.716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

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**ORIGIN**

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AW853610  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
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ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT

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AW853610.1  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 536)  
Dias Neto,A., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A.E., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the expressed human genome

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This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
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High quality sequence stop: 535.
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/note="Organ: colon; Vector: puc18; Site_1: SmA1; Site_2:
SmA1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
140 a 123 c 129 g 144 t

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into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
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QY      286  tacaaccaaccgagcctgtgaagtcctctctctaccacagccagctggcgaggaac 345
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QY      346  tccaccttgagctctgtggcctttccctggctgggttcctgcctgcagctctctgaaggaggc 405
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RESULT 12
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DEFINITION mRNA sequence.
ACCESSION BF244205
VERSION BF244205.1 GI:11158135
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@femail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LINC941 row: k column: 12
High quality sequence stop: 582.
FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:408099"
/tissue_type="NIH_MGC_57"
/lab_host="DH10B (TI phage-resistant)"
/notes="Organ: brain; Vector: pDNR-LIB (Clontech); Site: 1:
SfiI (ggccctcgcc); Site 2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATTAGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 256 a 216 c 171 g 227 t
ORIGIN
Query Match 23.7%; Score 113.2; DB 10; Length 870;
Best Local Similarity 58.2%; Pred. No. 5.1e-23;
Matches 199; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

Qy 136 ttaatctatgccgacatgtggagacccttgagaaagacagagggaccccatctacctg 195
Db 5 TTAATAGGCTGTAGACACACAGAATTCAGTGACAAAGGAAAGGGTATATGTTTACCTG 64

Qy 196 ggcctgaatgactcaatctctgctgatgtgtcgttaaagtgcgggaccagccacactg 255
Db 65 GGAATCAGGGAAAGATCTCTGTCTCTGTGCAGAAATTCAGGCGCAAGCCCTACTTGT 124
Qy 256 cagctgaaggaagaaatgaatgattgtacaaccaaccgacgctgtgaagtccttt 315
Db 125 CAGCTTAAGGAAAAAATATCATGTGACCTGTATGTGGAGAAGAAAGACAGAGAGCCCTTT 184

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Qy 316 ctcttaccacagcagagtgccaggaactccacctctgagctgtggtcttccctggc 375
Db 185 CTCCTTTTCCACATATAGAGAGGCTCCACTCTCTGCTTTTCAGTCAGTCCTTACCTGGC 244
Qy 376 tgggtcatcgctgcagctctgaaggagggtgctctctctatcctctaccacgaactgggg 435
Db 245 TGGTTCATAGCCACTCCACCACATCAGACAGCCCATCTTTCTCACCAGGAGAGAGGC 304
Qy 436 aaagcccaactactgactgtggttaactatgctgttttaa 477
Db 305 ATAACTAATACACTACTTCTTCTACTTATGATCTGTGGAATA 346

RESULT 13
AW753217/c 434 bp mRNA linear EST 28-APR-2000
LOCUS RC1-CT0251-081099-011-a04 CT0251 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW753217
ACCESSION AW753217
VERSION AW753217.1 GI:7668149
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0251-
081099-011-a04&t3=1999-10-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 42
High quality sequence stop: 67.
FEATURES
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1. .434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0251"
/dev_stage="Adult"
/notes="Organ: colon; Vector: puc18; Site: 1: SmaI; Site: 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 125 a 94 c 101 g 114 t
ORIGIN
Query Match 23.3%; Score 111; DB 9; Length 434;
Best Local Similarity 71.6%; Pred. No. 1.6e-22;
Matches 174; Conservative 0; Mismatches 65; Indels 4; Gaps 2;

Qy 226 tttgctaaagtcgggagccagccacactgcagctgaagaaaggata-taatggattt 284

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Db	21	GTATGTGAAAGGTTGGACAAAGCCCATATGCAAGTTCAGAGAGAGACGATCATCTGGATCT	80
Qy	285	gtacaaccaaccgagctgtgaagtcctcttcttaccacagccagagtggcagaaa	344
Db	81	GTATGGGCACAACGAGCCGTGAACCCCTTCCCTTGTCACCGGGCAAGACTGGTAGGAC	144
Qy	345	ctccaccttcagctgtctgggttttccctgagctggtttcatcgtgtcaactctgaagagg	404
Db	141	CTCCACCCCTTGAGTCTGTGGGCTTTCCTGGGACTGGTTCATCGC---CTCCTCCACAGAGAGA	199
Qy	405	cigtctctcatccttaccacaagaactggggaagccaacactactgactttggggttaac	464
Db	198	CCAGCCCATCTTCGACTTCAGAACTCGGGAAGTCATACAACACTGCCCTTTGAATTAAA	257
Qy	465	tat	467
Db	258	TAT	260

RESULT	15
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LOCUS	30257579F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:448603
DEFINITION	mRNA sequence.
ACCESSION	BG245180
VERSION	BG245180
KEYWORDS	GI:12754995
SOURCE	EST.
ORGANISM	house mouse.
	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
REFERENCE	1 (bases 1 to 1020)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

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DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLML0328 row: n column: 19
High quality sequence start: 4
High quality sequence stop: 653.
Location/Qualifiers
1..1020
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4486098"
/clone_lib="NCI CGAP Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
282 a 269 c 268 g 201 t

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[illegible]

Qy	248	ccacactgcagctgaaggaaaggatataatggatttgtacaaccaaccccgagcctgtga	307
Db	348	TCAAGCTCCAGCTGGAGGAAGTTACATCACTGATCTGAGCAAGACAAAGAGAGAGACA	407
Qy	308	agtcctttctcttaccacagccagagtggcaggaactccaccttcgagtcgtggttt	367
Db	408	AGCGCTTTACCTTCATCCGCTCTGAGAAAGGCCCCACCACGCTTTGAGTCAGCTGCCT	467
Qy	368	tccctggctggttcacgtgtcagctctgaaggaggtgtcctctcctcctaccacaag	427
Db	468	GTCCAGGATGGTTCCTCTGCACAACTAGAGGCTGACCGTCCCTGTGAGCCTCACCAACA	527
Qy	428	aactggggaaagcc	441
Db	528	CACCGGAAGAGCCC	541

Search completed: June 21, 2002, 11:09:02  
Job time: 17650 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:03:08 ; Search time 73.84 seconds  
(without alignments)  
237.671 Million cell updates/sec

Title: US-09-763-498-13

Perfect score: 830

Sequence: 1 MEKALIKDTPGSIQDINH.....ILTQELGKANTDGLTMLF 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	830	100.0	158	21	Human Interleukin-
2	826	99.5	158	21	Human Interleukin-
3	806	97.1	273	22	Human Interleukin-
4	646	77.8	130	22	Human Interleukin-
5	466.5	56.2	169	19	Human Interleukin-
6	466.5	56.2	169	20	Human Interleukin-
7	466.5	56.2	169	20	Human Interleukin-
8	466.5	56.2	169	22	Human Interleukin-
9	466.5	56.2	169	22	Human Interleukin-
10	466.5	56.2	173	22	Human Interleukin-
11	466.5	56.2	208	20	Human Interleukin-

12	463	55.8	157	22	Mouse interleukin-
13	463	55.8	160	19	Rodent interleukin
14	463	55.8	160	20	Amino acid sequenc
15	459.5	55.4	172	22	Human novel secret
16	459.5	55.4	172	22	Human gene 13 enco
17	389	46.9	170	22	Human interleukin-
18	384	46.3	157	22	Human Interleukin-
19	384	46.3	157	22	Human IL-1 eta. H
20	371	44.7	70	21	Partial human Inte
21	367.5	44.3	134	21	A novel polypeptid
22	367.5	44.3	134	21	Human IL-1 recepto
23	244.5	29.5	98	20	Amino acid sequenc
24	239	28.8	72	19	Rodent interleukin
25	214	25.8	218	21	Human zilla4-E200D
26	211	25.4	176	22	Human extracellular
27	210	25.3	163	21	Human IL-1 recepto
28	210	25.3	167	21	Human IL-1 recepto
29	210	25.3	192	21	Human interleukin-
30	210	25.3	193	22	Processed human IL
31	210	25.3	193	22	Human PRO3435. Ho
32	210	25.3	197	21	Human interleukin-
33	210	25.3	198	22	Interleukin-1 homo
34	210	25.3	203	21	Human IL-1R1a fuse
35	210	25.3	207	21	Human IL-1 recepto
36	210	25.3	218	21	Human interleukin-
37	210	25.3	218	21	Human IL-1 recepto
38	210	25.3	218	21	Human zilla4 prote
39	210	25.3	218	21	Human interleukin-
40	210	25.3	218	21	Primate interleuki
41	210	25.3	218	22	Human interleukin
42	210	25.3	218	22	Interleukin-1 homo
43	210	25.3	218	22	IL-1 related polyp
44	208	25.1	218	21	Human zilla4-E200k
45	205	24.7	218	21	Primate interleuki

## ALIGNMENTS

RESULT 1	
AA70218	AA70218 standard; Protein; 158 AA.
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XX	AA70218;
DT	06-JUN-2000 (first entry)
XX	Human Interleukin-1 epsilon polymorphic variant.
DE	
XX	Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW	Immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW	gene mapping; immune system; treatment; inflammatory disease;
KW	autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW	psoriasis; polymorphic variant; human.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Misc-difference 12
FT	/note= "Wild type Gln replaced with Arg"
XX	
PN	WO200011174-A1.
XX	
PD	02-MAR-2000.
XX	
PF	20-AUG-1999; 99WO-US18771.
XX	
PR	21-AUG-1998; 98US-0097413.
PR	31-AUG-1998; 98US-0098595.
PR	11-SEP-1998; 98US-0099974.
XX	
PA	(IMMV ) IMMUNEX CORP.
XX	

PI Sims JE, Smith DE;  
 XX WPI; 2000-237653/20.  
 DR N-PSDB; AAZ51248.  
 XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
 PT treat inflammatory and immune system-related diseases such as  
 PT rheumatoid arthritis and inflammatory bowel disease -  
 XX  
 PS Claim 1b; Fig 2; 76pp; English.  
 XX  
 CC The present protein sequence is that of human Interleukin-1 (IL-1)  
 CC epsilon polymorphic variant. IL-1 epsilon gene is mapped to chromosome 2q  
 CC and is mainly expressed in spleen, lymph node, thymus, tonsil and  
 CC leucocyte tissues. IL-1 epsilon is a cytokine, with antiinflammatory,  
 CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic  
 CC activity. It can be used in the treatment of inflammatory or autoimmune  
 CC diseases such as rheumatoid arthritis, inflammatory bowel disease and  
 CC psoriasis. The DNA sequence can be used in chromosome identification,  
 CC gene mapping and study of immune system.  
 XX  
 SQ Sequence 158 AA;  
 Query Match 100.0%; Score 830; DB 21; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-81;  
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEKALKIDTPQSGTQDINHRVWVLDOTLIAPVKRDMSPVTIALISCRHVETLEKDRG 60  
 DB 1 mekalidtpqgsiqdinhrvwlqdgqtliaavprkdrmsptvialisrhetlekdrg 60  
 QY 61 NPIYLGLNGLNCLMCAKVGDOPTQLKEKDMDLYNQPEPVKSFYHSQSGRNSTFES 120  
 DB 61 npilyglnglnclmcakvgdptqlkkekdimdlynqppepvksfifysqsggrnstfes 120  
 QY 121 VAPPGWFIAVSSEGGCPILLTQELGKANTTDFGLTMLF 158  
 DB 121 vaipgwfiavssggcpilltqelgkanttfdgltmlf 158  
 RESULT 2  
 AAY70217  
 ID AAY70217 standard; Protein; 158 AA.  
 XX  
 AC AAY70217;  
 XX  
 DT 06-JUN-2000 (first entry)  
 XX  
 DE Human Interleukin-1 epsilon protein.  
 XX  
 KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;  
 KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;  
 KW gene mapping; immune system; treatment; inflammatory disease;  
 KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;  
 KW psoriasis; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200011174-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US18771.  
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 PR 21-AUG-1998; 98US-0097413.  
 PR 31-AUG-1998; 98US-0098595.  
 PR 11-SEP-1998; 98US-0099974.  
 XX  
 PA (IMV ) IMMUNEX CORP.  
 XX  
 PI Sims JE, Smith DE;  
 XX

DR WPI; 2000-237653/20.  
 DR N-PSDB; AAZ51247.  
 XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to  
 PT treat inflammatory and immune system-related diseases such as  
 PT rheumatoid arthritis and inflammatory bowel disease -  
 XX  
 PS Claim 1b; Fig 2; 76pp; English.  
 XX  
 CC The present sequence is that of human Interleukin-1 (IL-1) epsilon  
 CC protein. IL-1 epsilon gene is mapped to chromosome 2q and is mainly  
 CC expressed in spleen, lymph node, thymus, tonsil and leucocyte  
 CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,  
 CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic  
 CC activity. It can be used in the treatment of inflammatory or autoimmune  
 CC diseases such as rheumatoid arthritis, inflammatory bowel disease and  
 CC psoriasis. The DNA sequence can be used in chromosome identification,  
 CC gene mapping and study of immune system.  
 XX  
 SQ Sequence 158 AA;  
 Query Match 99.5%; Score 826; DB 21; Length 158;  
 Best Local Similarity 99.4%; Pred. No. 1.4e-80;  
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 DB 1 mekalidtpqgsiqdinhrvwlqdgqtliaavprkdrmsptvialisrhetlekdrg 60  
 QY 61 NPIYLGLNGLNCLMCAKVGDOPTQLKEKDMDLYNQPEPVKSFYHSQSGRNSTFES 120  
 DB 61 npilyglnglnclmcakvgdptqlkkekdimdlynqppepvksfifysqsggrnstfes 120  
 QY 121 VAPPGWFIAVSSEGGCPILLTQELGKANTTDFGLTMLF 158  
 DB 121 vaipgwfiavssggcpilltqelgkanttfdgltmlf 158  
 RESULT 3  
 AAEO3417  
 ID AAEO3417 standard; Protein; 273 AA.  
 XX  
 AC AAEO3417;  
 XX  
 DT 03-AUG-2001 (first entry)  
 XX  
 DE Human interleukin-1 receptor antagonist-like (IL-lra-L).  
 XX  
 KW Human; interleukin-1 receptor antagonist-like protein; IL-lra-L; therapy;  
 KW rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;  
 KW joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;  
 KW transplant rejection; graft versus host disease; strain; sprain; leprosy;  
 KW cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;  
 KW clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;  
 KW myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;  
 KW acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;  
 KW eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;  
 KW hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;  
 KW infertility; endometriosis; retinal neuropathy; acute pancreatitis;  
 KW Kawasaki's disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200141792-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 04-DEC-2000; 2000WO-US32891.  
 XX  
 PR 10-DEC-1999; 99US-0170105.  
 PR 28-NOV-2000; 2000US-0724859.  
 XX

PA (AMGE-) AMGEN INC.  
XX Calzone EJ, Luethy R, Boedigheimer MJ, Zhu J, Chung Y, Jing S;  
PI  
XX  
XX  
XX WPI; 2001-381495/40.  
DR N-PSDB; AAD06911.  
XX  
XX Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the  
PT polypeptide encoded by the nucleic acid is useful diagnosis, treatment,  
PT and prevention of diseases such as arthritis, diabetes, transplant  
PT rejection  
XX  
XX Claim 13; Fig 1A; 127pp; English.  
PS  
XX  
XX The present sequence is human interleukin-1 receptor antagonist-like  
CC (IL-lra-L) protein. IL-lra-L is useful for treating, preventing or  
CC ameliorating IL-lra-L polypeptide-related disease, condition or disorder  
CC which include rheumatoid arthritis, psoriatic arthritis, inflammatory  
CC arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,  
CC lupus, diabetes, transplant rejection, inflammatory joint disease, graft  
CC versus host disease and inflammatory conditions resulting from strain,  
CC sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human  
CC immunodeficiency virus (HIV) infection, clostridium-associated  
CC diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,  
CC anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory  
CC disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,  
CC psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,  
CC Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,  
CC lymphomas, lung and breast cancer, leukaemia, infertility,  
CC endometriosis, retinal degeneration, retinal neuropathy, acute  
CC pancreatitis and Kawasaki's disease.  
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SQ Sequence 273 AA;  
  
Query Match 97.1%; Score 806; DB 22; Length 273;  
Best Local Similarity 99.4%; Pred. No. 3.9e-78;  
Matches 153; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 LKIDTPQGSTQDINHVRVWVLDQDTLAVPRKDRMSPVTALISCRHVETLEKDRGNPIY 64  
Db 120 lkidtpqgsiqdinhvrwvldqdtlavrprkdrmspvtaliscrhvetciekdrdgly 179  
  
QY 65 LGUNGLNCLMCAKVGQDPTLQLEKIDIMLYNQPEPVKSFLEYHSQSGRNSTFESVAFP 124  
Db 180 lginglnclmcakvqgqptlqlekdmdlynpqpepvksflfyhsqsgrnstfesvaif 239  
  
QY 125 GWFTAVSSEGGCPILITQELGKANTDFGLTMLF 158  
Db 240 gwftavsssegcpililtqelgkanttfdgltmif 273  
  
RESULT 4  
AAB85001  
ID AAB85001 standard; Protein; 130 AA.  
XX  
XX AAB85001;  
XX  
XX 06-AUG-2001 (first entry)  
XX  
XX Human interleukin-1 receptor antagonist (NOVINTRA C) polypeptide.  
XX  
XX NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;  
XX gonadotropin-like protein; NOVGON; interleukin-1; NOVINTR A; human;  
XX cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;  
XX antibacterial; cerebroprotective; antidiabetic; antiarthritic;  
XX antiasthmatic; antiallergic.  
XX  
XX Homo sapiens.  
XX  
XX WO200140291-A2.  
XX  
XX 07-JUN-2001.  
PD

XX  
PF 06-DEC-2000; 2000WO-US33029.  
XX  
XX 06-DEC-1999; 99US-0169056.  
PR 09-DEC-1999; 99US-0169866.  
PR 09-DEC-1999; 99US-0169886.  
PR 10-DEC-1999; 99US-0170252.  
PR 12-JAN-2000; 2000US-0175740.  
PR 05-DEC-2000; 2000US-0170252.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Burgess CE, Prayaga SK, Shimkets RA, Rastelli L, Zerhusen BD;  
PI Mezes PS;  
XX  
XX WPI; 2001-374790/39.  
DR N-PSDB; AAF83870.  
XX  
XX Novel isolated human transmembrane, neuromedin peptide  
PT gonadotropin-like protein and interleukin-1 receptor antagonist  
PT proteins, useful for treating cancer, immune response disorder,  
PT metabolic function disorders  
XX  
XX Claim 53; Fig 15B; 138pp; English.  
XX  
XX The invention provides novel polypeptides (NOVX) selected from human  
CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),  
CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor  
CC antagonist proteins (NOVINTRA A and B). The invention also provides  
CC methods in which a NOVX polypeptide, polynucleotide and antibody are  
CC used in the detection, prevention and treatment of a broad range of  
CC pathological states. NOVTRAN can be used to treat a cell signaling  
CC disorder such as cancer, immune response disorder, hematopoietic  
CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat  
CC endocrine disorder, muscle disorder, neurologic disorder, cancers of  
CC central nervous system, breast, colon, ovary, kidney, prostate and  
CC thyroid. NOVGON can be used to treat reproductive development disorder,  
CC metabolic function disorder and melanoma. NOVINTR A and B can be used  
CC to treat bone metabolism or structure disorder, inflammatory response  
CC disorder, immune regulation disorder, septic shock, diabetes,  
CC arthritis and cancer. The present sequence represents the NOVINTR A  
CC polypeptide.  
XX  
SQ Sequence 130 AA;  
  
Query Match 77.8%; Score 646; DB 22; Length 130;  
Best Local Similarity 95.5%; Pred. No. 2.1e-61;  
Matches 126; Conservative 1; Mismatches 1; Indels 4; Gaps 2;  
  
QY 17 DINHRVWVLDQDTLAVPRKDRMSPVTALISCRHVETLEKDRGNPIYGLNGLNCLMC 76  
Db 1 dinhrvwwldqdtlavrprk--vfpvtaliscrhvetciekdrngpiylgnglnclmc 58  
  
QY 77 AKVGQDPTLQLEKIDIMLYNQPEPVKSFLEYHSQSGRNSTFESVAFPGWFTAVSSEG 134  
Db 59 akvgdqptlqlekdmdlynpqpepvksflfyhsqsgrnstfesvaifpgwftavssseg 118  
  
QY 135 GCPILITQELGK 146  
Db 119 gcpliltqelgk 130  
  
RESULT 5  
AAW63136  
ID AAW63136 standard; Protein; 169 AA.  
XX  
XX AAW63136;  
XX  
XX 14-OCT-1998 (first entry)  
XX  
XX Interleukin-1 receptor antagonist beta (IL-lra-beta).  
DE  
XX



RESULT	8
AAE06656	
ID	AAE06656 standard; Protein; 169 AA.
XX	
AC	AAE06656;
XX	
DT	16-OCT-2001 (first entry)
XX	
DE	Human interleukin-lepsilon (IL-lepsilon) protein.
XX	
KW	Human; interleukin-lepsilon; IL-lepsilon; virucide; hepatotropic; fever;
KW	immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW	autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW	psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
Binding-site	17..20
FT	/note= "IL-1 receptor beta subunit binding region"
FT	23
Binding-site	/note= "IL-1 receptor beta subunit binding region"
FT	23..27
Region	/note= "Beta sheet region"
FT	28
Binding-site	/note= "IL-1 receptor alpha subunit binding region"
FT	30..32
Binding-site	/note= "IL-1 receptor alpha subunit binding region"
FT	34..36
Region	/note= "Beta sheet region"
FT	36..38
Binding-site	/note= "IL-1 receptor alpha subunit binding region"
FT	42..45
Region	/note= "Beta sheet region"
FT	43
Binding-site	/note= "IL-1 receptor alpha subunit binding region"
FT	45..50
Binding-site	/note= "IL-1 receptor alpha subunit binding region"
FT	52
Binding-site	/note= "IL-1 receptor alpha subunit binding region"
FT	56..61
Region	/note= "Beta sheet region"
FT	61
Binding-site	/note= "IL-1 receptor beta subunit binding region"
FT	63
Binding-site	/note= "IL-1 receptor beta subunit binding region"
FT	68
Binding-site	/note= "IL-1 receptor beta subunit binding region"
FT	70..71
Binding-site	/note= "IL-1 receptor beta subunit binding region"
FT	73
Binding-site	/note= "IL-1 receptor beta subunit binding region"
FT	73..97
Binding-site	/note= "IL-1 receptor alpha subunit binding region"
FT	74..79
Region	/note= "Beta sheet region"
FT	84..89
Region	/note= "Beta sheet region"
FT	

Query Match 56.2%; Score 466.5; DB 20; Length 169;

FT Region /note= "Beta sheet region"  
 FT 96..101  
 FT /note= "Beta sheet region"  
 FT 110..112  
 FT Binding-site /note= "IL-1 receptor beta subunit binding region"  
 FT 117..122  
 FT Region /note= "Beta sheet region"  
 FT 121  
 FT Binding-site /note= "IL-1 receptor beta subunit binding region"  
 FT 123..124  
 FT Binding-site /note= "IL-1 receptor beta subunit binding region"  
 FT 126..127  
 FT Binding-site /note= "IL-1 receptor beta subunit binding region"  
 FT 129..132  
 FT Region /note= "Beta sheet region"  
 FT 138..142  
 FT Region /note= "Beta sheet region"  
 FT 144..145  
 FT Binding-site /note= "IL-1 receptor alpha subunit binding region"  
 FT 147..148  
 FT Binding-site /note= "IL-1 receptor alpha subunit binding region"  
 FT 148..152  
 FT Region /note= "Beta sheet region"  
 FT 159..167  
 FT Region /note= "Beta sheet region"  
 FT 164  
 FT Binding-site /note= "IL-1 receptor alpha subunit binding region"  
 FT 166  
 FT Binding-site /note= "IL-1 receptor alpha subunit binding region"  
 FT 167  
 FT Binding-site /note= "IL-1 receptor beta subunit binding region"  
 FT 169  
 FT Binding-site /note= "IL-1 receptor beta subunit binding region"  
 FT WO200157219-A2.  
 PN WO200157219-A2.  
 XX 09-AUG-2001.  
 XX 01-FEB-2001; 2001WO-US03285.  
 XX 02-FEB-2000; 2000US-0179638.  
 XX (SCHE ) SCHERING CORP.  
 PA Debets JEMA, Timans JC, Bazan JF, Kastelein RA;  
 PI WPI: 2001-48886/53.  
 DR N-PSDB: AAD12296.  
 XX Novel isolated or recombinant antigenic interleukin-1 delta or epsilon  
 PT polypeptide useful for treating conditions exhibiting abnormal  
 PT expression of interleukin such as immunological disorders, tumor and  
 PT allergy -  
 XX Claim 18; Fig 1; 103pp; English.  
 PS The invention relates to recombinant antigenic interleukin-1 like  
 CC molecules and their corresponding nucleic acid sequences, designated  
 CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).  
 CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting  
 CC abnormal expression of the interleukin such as immunological disorders,  
 CC tumours, inflammatory diseases, fever, hypoglycaemia, psoriasis,  
 CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary  
 CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as  
 CC HIV). The invention also relates to methods of using the composition  
 CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic  
 CC antisera or antibodies specific, e.g., capable of distinguishing between  
 CC IL-1 family members and an IL-1delta, for the interleukin or its  
 CC fragment. The purified interleukin is used as a reagent to detect any  
 CC antibodies generated in response to the presence of elevated levels of  
 CC expression, or immunological disorders which lead to antibody production  
 CC to the endogenous cytokine. The invention also contemplates the use of

CC competitive drug screening assays. The present sequence is human  
 CC interleukin-1epsilon (IL-1epsilon) protein.  
 XX SQ Sequence 169 AA;  
 Query Match 56.2%; Score 466.5; DB 22; Length 169;  
 Best Local Similarity 59.9%; Pred. No. 5.1e-42;  
 Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;  
 QY 10 PQRSGIQDINIRVWVLDQDTLIAVPRKDRMSPVTIALISCRHVTLEKDRGNPIYVLGNG 69  
 Db 22 pitgtindinqvwcilgqnlvavprsdvtpvtvavtkypaaleqgrdpylgqn 81  
 QY 70 LNLCLMCAKVGSDQPTLQLKEKDMDLYNQPEPVKSFLFYHSQSRNSTFESVAFPGWFA 129  
 Db 82 pemclycekvgqetlqlkeqkimdlylqgpevpkpflyraktgtstlesvafpdwfa 141  
 QY 130 VSSEGCGPLLTLQELGKANTTDFGLTM 156  
 Db 142 -sskrdgpiltselgksyntafeini 167  
 RESULT 9  
 AAB83008  
 ID AAB83008 standard; protein: 169 AA.  
 XX AC AAB83008;  
 XX 21-JUN-2001 (first entry)  
 XX Human IL-1ra protein.  
 DE Human; IL-1ra; interleukin-1 receptor antagonist; antibacterial;  
 XX immunosuppressive; antiinflammatory; antiarthritic; nephrotropic;  
 KW hepatotropic; virucide; cardiant; vasotropic; antidiabetic; cancer;  
 KW neuroprotective; osteopathic; cytostatic; immunomodulator; nootropic;  
 KW cerebroprotective; antidepressant; antiarteriosclerotic; infection;  
 KW immune disease; autoimmune disease; bone disease; neuronal disease;  
 KW cardiovascular disease.  
 XX OS Homo sapiens.  
 XX WO200119390-A1.  
 PN 22-MAR-2001.  
 XX 28-AUG-2000; 2000WO-IB01192.  
 XX 14-SEP-1999; 99US-0154010.  
 XX (PFIZ ) PFIZER PROD INC.  
 PA Littman BH, Woodworth TLG, Dombroski MA;  
 XX WPI: 2001-327986/34.  
 DR Synergistic treatment of interleukin (IL)-mediated diseases, useful for  
 XX e.g. septic shock, comprises adjunctively administering IL-1 receptor  
 PT antagonist polypeptide and non-steroidal IL-1 processing and release  
 PT inhibiting agent -  
 XX Disclosure; Page 91; 112pp; English.  
 PS The present sequence is a human interleukin-1 receptor antagonist  
 CC (IL-1ra). The present sequence or its variant may be administered  
 CC in combination with a non-steroidal IL-1 processing and release  
 CC inhibiting agent for the treatment or prevention of IL-mediated disease  
 CC states. The composition is useful for treating inappropriate host  
 CC responses to infectious diseases where active infection exists at any  
 CC body site, e.g. septic shock, disseminated intravascular coagulation,  
 CC and/or adult respiratory distress syndrome; acute or chronic  
 CC inflammation due to antigen, antibody and/or complement deposition;

CC inflammatory conditions including arthritis, cholangitis, colitis,  
 CC encephalitis, endocarditis, glomerulonephritis, hepatitis, myocarditis,  
 CC pancreatitis, pericarditis, and reperfusion injury vasculitis. It is  
 CC also useful for treating immune-based diseases including conditions  
 CC involving T cells and/or macrophages e.g. acute and delayed  
 CC hypersensitivity, graft rejection, graft-versus-host disease;  
 CC autoimmune diseases including Type I diabetes mellitus and multiple  
 CC sclerosis. The composition may be used for treating bone and cartilage  
 CC resorption as well as diseases resulting in excess deposition of  
 CC extracellular matrix. Such diseases include osteoporosis, periodontal  
 CC diseases, interstitial pulmonary fibrosis, cirrhosis, systemic sclerosis  
 CC and keloid formation. It is also useful for treating tumours which  
 CC produce IL-1 as an autocrine growth factor and for preventing the  
 CC cachexia associated with certain tumours. It may be used for  
 CC treating neuronal diseases with an inflammatory component e.g.  
 CC Alzheimer's disease, stroke, depression and percussion injury and for  
 CC cardiovascular diseases in which recruitment of monocytes into the  
 CC subendothelial space plays a role, e.g. the development of  
 CC atherosclerotic plaques.

XX  
 SQ Sequence 169 AA;

Query Match 56.2%; Score 466.5; DB 22; Length 169;  
 Best Local Similarity 59.9%; Pred. No. 5.1e-42;

Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;

QY 10 PQRGSIQDINHRVWLDQTLIAVPRKDRMSPVTIALISCRHVTLEKDRGNPIYIGLNG 69

Db 22 pitgtindlqqwvltgqnlvavrsdsvtvcvavtkypealeqrgdplyigqn 81

QY 70 LNLCLMCAKVGDDQTLQLEKIDIMLYNQPEPVKSFIFYHSQSGRNSTFESVAFPGWFIA 129

Db 82 pemclcyekvgeptlqlkeqkmdlygqepvpkpflyfraktgrtstlesvafpawfia 141

QY 130 VSSGGGCLLIITQELGKANTWDFGLTW 156

Db 142 -sskrdpilltseigksyntafelni 167

RESULT 10

AAU16937

ID AAU16937 standard; Protein; 173 AA.

XX AC AAU16937;

XX DT 07-NOV-2001 (first entry)

XX DE Human novel secreted protein, SEQ ID 178.

XX KW Human; immunosuppressive; antiarthritic; antirheumatic;  
 KW cytotatic; cardiant; vasotropic; cerebroprotective; nootropic;  
 KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
 KW vulnery; secreted protein; rheumatoid arthritis;  
 KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
 KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;  
 KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
 KW corneal infection; wound healing; epithelial cell proliferation;  
 KW skin ageing; food additive; preservative; antiproliferative.

XX OS Homo sapiens.

XX PN WO200155441-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01320.

XX PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-JUL-2000; 2000US-0218290.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR 26-JUL-2000; 2000US-0220964.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR 14-AUG-2000; 2000US-0225213.  
 PR 14-AUG-2000; 2000US-0225214.  
 PR 14-AUG-2000; 2000US-0225266.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 14-AUG-2000; 2000US-0225759.  
 PR 18-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226688.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0232400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 21-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235836.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.





XX Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;  
 KW Inflammatory response; immune system; diagnosis; agonist; antagonist;  
 KW Chemokine.  
 OS Mus sp.  
 XX WO9847921-A1.  
 PN 29-OCT-1998.  
 XX 17-APR-1998; 98WO-US06879.  
 XX 06-AUG-1997; 97US-0055111.  
 PR 21-APR-1997; 97US-0837627.  
 XX (SCHE ) SCHERING CORP.  
 PA Bazan JF, Hedrick JA, Kastelein RA, Sana TR;  
 PI WPI; 1998-609976/51.  
 DR N-PSDB; AAV71960.  
 XX Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.  
 PT regulating the immune system and inflammatory responses  
 XX Claim 1; Pages 92-93; 113pp; English.  
 CC This represents a rodent interleukin (IL)-1 epsilon polypeptide. The  
 CC invention relates to a recombinant polypeptide that specifically binds  
 CC polyclonal antibodies (Abs) generated against a 12 consecutive amino acid  
 CC segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these  
 CC IL polypeptides are used to regulate a cell involved in an inflammatory  
 CC response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are  
 CC used to produce Abs and antigen-Abs complexes. The polypeptides, Abs and  
 CC the corresponding nucleic acids regulate development and/or the immune  
 CC system, and can be used to diagnose and treat conditions associated with  
 CC abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1  
 CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,  
 CC IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1  
 CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion  
 CC protein with another cytokine or chemokine.  
 XX Sequence 160 AA;  
 SQ  
 Query Match 55.8%; Score 463; DB 19; Length 160;  
 Best Local Similarity 54.5%; Pred. No. 1.1e-41;  
 Matches 85; Conservative 30; Mismatches 41; Indels 0; Gaps 0;  
 QY 2 EKALKIDTPQGSIQDINHRYVWLQDOTLIAVPRKDRMSPTVIALISCRHVETLEKDRGN 61  
 DB 4 ekelraaspslrhvqdlssrwiqlnlltavprkeqcvptitlpcqyldtletrgd 63  
 QY 62 PYYGLNGLNLCIMCAKVGDDPTLQLKEKDIMDLYNQPEPVKSLFYHSQSGRNSTFESV 121  
 DB 64 ptymgvgrpmcsclctkdqegvqlqgegnimemynkpevkaslfyhksgtstfesa 123  
 QY 122 APFGWFIAVSSGGCPILITOTELGKANTTDFGLTML 157  
 DB 124 apfgwfiavcskgscllittqei9iftdremilvv 159  
 RESULT 14  
 ID AAY24049  
 AC AAY24049 standard; Protein; 160 AA.  
 XX AAY24049;  
 AC AAY24049;  
 XX 30-SEP-1999 (first entry)  
 DT Amino acid sequence of a murine SPOIL-II protein.  
 DE  
 XX

KW SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;  
 KW bone metabolism disorder; proinflammatory disorder; immune disorder;  
 KW inflammatory disease; septic shock; stroke; diabetes; arthritis;  
 KW intercolitis; pneumonitis; epithelial cell; skin disease;  
 KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;  
 KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;  
 KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;  
 KW osteogenesis imperfecta; fibrous dysplasia; hypophosphatasia;  
 KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;  
 KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;  
 KW bone fracture.  
 XX Mus sp.  
 OS WO9937662-A1.  
 PN 29-JUL-1999.  
 XX 26-JAN-1999; 99WO-US01575.  
 PD 27-JAN-1998; 98US-0013810.  
 XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 PA Busfield SJ;  
 PI WPI; 1999-458675/38.  
 DR N-PSDB; AAX86460.  
 XX New isolated SPOIL proteins, used to develop products for treating,  
 PT e.g. inflammatory and immune disorders  
 XX Claim 8; Fig 6; 126pp; English.  
 CC The present sequence represents a SPOIL-II protein. SPOIL proteins have  
 CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.  
 CC The SPOIL proteins are used as modulating agents in regulating a variety  
 CC of cellular processes. The products can be used for treating disorders  
 CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone  
 CC metabolism disorder, a proinflammatory disorder or an immune disorder.  
 CC They can be used for treating e.g. inflammatory diseases and disorders  
 CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,  
 CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and  
 CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma  
 CC and Kaposi's sarcoma and other epithelial cancers including squamous cell  
 CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and  
 CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's  
 CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,  
 CC fibrous dysplasia, hypophosphatasia, bone sarcoma, myeloma bone disorder  
 CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and  
 CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in  
 CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.  
 CC decrease bone fragility); and prevention and/or treatment of bone pain,  
 CC bone deformities and/or bone fractures. The products can also be used for  
 CC detection, diagnosis and screening assays.  
 XX Sequence 160 AA;  
 SQ

Query Match 55.8%; Score 463; DB 20; Length 160;  
 Best Local Similarity 54.5%; Pred. No. 1.1e-41;  
 Matches 85; Conservative 30; Mismatches 41; Indels 0; Gaps 0;  
 QY 2 EKALKIDTPQGSIQDINHRYVWLQDOTLIAVPRKDRMSPTVIALISCRHVETLEKDRGN 61  
 DB 4 ekelraaspslrhvqdlssrwiqlnlltavprkeqcvptitlpcqyldtletrgd 63  
 QY 62 PYYGLNGLNLCIMCAKVGDDPTLQLKEKDIMDLYNQPEPVKSLFYHSQSGRNSTFESV 121  
 DB 64 ptymgvgrpmcsclctkdqegvqlqgegnimemynkpevkaslfyhksgtstfesa 123  
 QY 122 APFGWFIAVSSGGCPILITOTELGKANTTDFGLTML 157  
 DB 124 apfgwfiavcskgscllittqei9iftdremilvv 159

Db 124 afgwfiavcsgscpllltqelgtfdmiv 159

RESULT 15

AAU17010

ID AAU17010 standard; Protein; 172 AA.

XX

XX AAU17010;

XX

XX 07-NOV-2001 (first entry)

XX Human novel secreted protein, SEQ ID 251.

XX Human; immunosuppressive; antiarthritic; antirheumatic;

KW cytotstatic; cardiant; vasotropic; cerebroprotective; nootropic;

KW neuroprotective; antibacterial; viruicide; fungicide; ophthalmological;

KW vulnery; secreted protein; rheumatoid arthritis;

KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;

KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;

KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;

KW corneal infection; wound healing; epithelial cell proliferation;

KW skin ageing; food additive; preservative; antiproliferative.

XX

OS Homo sapiens.

XX

PN WO20015441-A2.

XX

PD 02-AUG-2001.

XX

XX 17-JAN-2001; 2001WO-US01320.

PF

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0188874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 11-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 14-AUG-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

PR 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.

PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.

PR 05-SEP-2000; 2000US-0229513.

PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.

PR 08-SEP-2000; 2000US-0231242.

PR 08-SEP-2000; 2000US-0231243.

PR 08-SEP-2000; 2000US-0231244.

PR 08-SEP-2000; 2000US-0231413.

PR 08-SEP-2000; 2000US-0231414.

PR 08-SEP-2000; 2000US-0232081.

PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0231968.

PR 14-SEP-2000; 2000US-0232397.

PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0232399.

PR 14-SEP-2000; 2000US-0232400.

PR 14-SEP-2000; 2000US-0232401.

PR 14-SEP-2000; 2000US-0233063.

PR 14-SEP-2000; 2000US-0233064.

PR 14-SEP-2000; 2000US-0233065.

PR 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-0234223.

PR 25-SEP-2000; 2000US-0234997.

PR 25-SEP-2000; 2000US-0234998.

PR 25-SEP-2000; 2000US-0234998.

PR 26-SEP-2000; 2000US-0235484.

PR 27-SEP-2000; 2000US-0235834.

PR 27-SEP-2000; 2000US-0235836.

PR 29-SEP-2000; 2000US-0236327.

PR 29-SEP-2000; 2000US-0236367.

PR 29-SEP-2000; 2000US-0236368.

PR 29-SEP-2000; 2000US-0236369.

PR 29-SEP-2000; 2000US-0236370.

PR 02-OCT-2000; 2000US-0236802.

PR 02-OCT-2000; 2000US-0237037.

PR 02-OCT-2000; 2000US-0237038.

PR 02-OCT-2000; 2000US-0237039.

PR 02-OCT-2000; 2000US-0237040.

PR 13-OCT-2000; 2000US-0239935.

PR 13-OCT-2000; 2000US-0239937.

PR 20-OCT-2000; 2000US-0240960.

PR 20-OCT-2000; 2000US-0241221.

PR 20-OCT-2000; 2000US-0241785.

PR 20-OCT-2000; 2000US-0241786.

PR 20-OCT-2000; 2000US-0241787.

PR 20-OCT-2000; 2000US-0241808.

PR 20-OCT-2000; 2000US-0241809.

PR 20-OCT-2000; 2000US-0241826.

PR 01-NOV-2000; 2000US-0244617.

PR 08-NOV-2000; 2000US-0246474.

PR 08-NOV-2000; 2000US-0246475.

PR 08-NOV-2000; 2000US-0246476.

PR 08-NOV-2000; 2000US-0246477.

PR 08-NOV-2000; 2000US-0246478.

PR 08-NOV-2000; 2000US-0246523.

PR 08-NOV-2000; 2000US-0246524.

PR 08-NOV-2000; 2000US-0246525.

PR 08-NOV-2000; 2000US-0246526.

PR 08-NOV-2000; 2000US-0246527.

PR 08-NOV-2000; 2000US-0246528.

PR 08-NOV-2000; 2000US-0246532.

PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.

PR 08-NOV-2000; 2000US-0246611.

PR 08-NOV-2000; 2000US-0246613.

PR 17-NOV-2000; 2000US-0249207.

PR 17-NOV-2000; 2000US-0249208.

PR 17-NOV-2000; 2000US-0249209.

PR 17-NOV-2000; 2000US-0249210.

PR 17-NOV-2000; 2000US-0249211.

PR 17-NOV-2000; 2000US-0249212.

PR 17-NOV-2000; 2000US-0249213.

PR 17-NOV-2000; 2000US-0249214.

PR 17-NOV-2000; 2000US-0249215.

PR 17-NOV-2000; 2000US-0249216.

PR 17-NOV-2000; 2000US-0249217.

Fri Jun 21 14:40:26 2002

Db 146 -sskrdqpiiltseixksyntafelni 171  
Search completed: June 20, 2002, 15:03:08  
Job time: 119 sec

PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 17-NOV-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251866.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 11-DEC-2000; 2000US-0251990.  
PR 05-JAN-2001; 2001US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
DR WPI: 2001-476222/51.  
DR N-PSDB; AAS26915.  
XX  
XX  
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to  
PT diagnose diseases or disorders associated with aberrant expression or  
PT activity of polypeptides, for treating blood clotting disorder,  
PT haemophilia  
XX  
PS Claim 11; SEQ ID No 251; 601pp; English.  
XX  
XX The invention relates to isolated nucleic acid molecules and their  
CC encoded secreted proteins. The nucleic acids and proteins are used to  
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They  
CC are also used in diagnosing a pathological condition or susceptibility  
CC to a pathological condition. Antibodies to the proteins can also  
CC be used in alleviating symptoms associated with the disorders and in  
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated  
CC include autoimmune diseases e.g. rheumatoid arthritis,  
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
CC and ocular disorders e.g. corneal infection, and many other  
CC disorders listed in the specification. The polypeptides can also  
CC be used to aid wound healing and epithelial cell proliferation, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
CC as a food additive or preservative to increase or decrease storage  
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
CC minerals, cofactors and other nutritional components. The present  
CC

Query Match 55.4%; Score 459.5; DB 22; Length 172;  
Best Local Similarity 59.2%; Pred. No. 3e-41;  
Matches 87; Conservative 24; Mismatches 35; Indels 1; Gaps 1;  
Qy 10 PORGSIODINHRVWVLODQTLIAVPRKDRMSPTTIALISCRHVETLEKDRGNPIYLGNG 69  
Db 26 pitgtindlnqgvvtlqgqnlvavprsdsvtptvavtckypealeqgrgdpiylgqn 85  
Qy 70 LNLCLMCAKVGQPTLQLEKEDIMDLNQNPEPVKSFLEYHSQSGRNTFFESVAPPGWFIA 129  
Db 86 pemcylcekvgeqptlqlkeqkmdlygqpepvkpflyfraktgrtstlesvafpdwfa 145  
Qy 130 VSEGGCCPLIILTQELGRANTTDFGLTM 156





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 20, 2002, 15:03:52 ; Search time 36.86 Seconds  
(without alignments)  
411.886 Million cell updates/sec

Title: US-09-763-498-13

Perfect score: 830

Sequence: 1 MEKALKIDTPQSGSIODINH.....ILTQELGRANTDFGLTMLF 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Watch 0%

Maximum Watch 100%

Listing first 45 summaries

Database :

PIR\_71:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195.5	23.6	178	2 A44610	interleukin-1 rece
2	190.5	23.0	178	2 C40956	interleukin-1 rece
3	185.5	22.3	155	2 JC7104	interleukin-1 rece
4	183.5	22.1	177	2 A30368	interleukin-1 rece
5	183.5	22.1	180	2 A30385	interleukin-1 rece
6	173.5	20.9	266	1 S23010	interleukin-1 beta
7	170.5	20.5	177	2 AS4377	interleukin-1 rece
8	169.5	20.4	266	1 IC801B	interleukin-1 beta
9	159.5	19.2	267	2 S38373	interleukin-1 beta
10	155	18.7	267	1 JN0724	interleukin-1 beta
11	143.5	17.3	269	1 ICHU1B	interleukin-1 beta
12	141.5	17.0	268	1 A30584	interleukin-1 beta
13	137.5	16.6	214	2 JC5646	interleukin-1 beta
14	121	14.6	269	1 I55969	interleukin-1 beta
15	81	9.8	256	2 F86463	hypothetical prote
16	78	9.4	407	2 T22554	hypothetical prote
17	78	9.4	501	2 AG0939	glycerol kinase (l
18	77	9.3	268	1 IC801A	interleukin-1 alph
19	77	9.3	268	1 A61246	interleukin-1 alph
20	76	9.2	502	1 K1ECGL	glycerol kinase (E
21	76	9.2	502	2 C91235	glycerol kinase (l
22	76	9.2	509	2 C86082	glycerol kinase (l
23	75.5	9.1	270	1 S10532	interleukin-1 alph
24	74	8.9	15281	2 S41309	cyclosporin synthe
25	73.5	8.9	1320	2 H64090	phosphoribosylform
26	73	8.8	403	2 AC2271	precorrin-6y-depen
27	73	8.8	837	2 T48407	hypothetical prote
28	72.5	8.7	325	2 E87125	ribonucleotide red
29	72	8.7	1132	2 T43483	translation initia

30	71.5	8.6	325	2 S48698	3-dehydroquinatate d
31	71.5	8.6	421	2 A47713	chitin deacetylase
32	71	8.6	1426	2 T30817	homeotic protein C
33	70.5	8.5	270	2 I46620	interleukin-1 alph
34	70.5	8.5	460	2 AG2262	hypothetical prote
35	70.5	8.5	556	2 A44441	B-cell antigen CD1
36	70.5	8.5	944	2 G86720	translation initia
37	70.5	8.5	1077	2 T01474	hypothetical prote
38	70.5	8.5	1093	2 T51503	valine--trna ligas
39	70	8.4	447	2 H97146	siderophore/Surfac
40	70	8.4	516	2 H84424	probable MAP kinas
41	70	8.4	1057	2 T46193	hypothetical prote
42	69.5	8.4	454	2 G70476	conserved hypotet
43	69	8.3	327	1 OMPSY	ornithine carbamoy
44	69	8.3	501	1 VGEMA	glycoprotein A pre
45	69	8.3	501	1 A60005	glycoprotein A pre

#### ALIGNMENTS

##### RESULT 1

A44610  
interleukin-1 receptor antagonist precursor - mouse  
N: Alternate names: IL-1ra  
C: Species: Mus musculus (house mouse)  
C: Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 16-Jul-1999  
C: Accession: A44610; B40956; A49031; I56106; I52970  
R: Matsushime, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.  
Blood 78, 616-623, 1991  
A: Title: Cloning and expression of murine interleukin-1 receptor antagonist in macroph  
A: Reference number: A44610; MUID: 91316273  
A: Accession: A44610  
A: Molecule type: mRNA  
A: Residues: 1-178 <MAT>  
A: Cross-references: GB:M64404; NID: g198296; PIDN: AAA39277.1; PID: g198297  
R: Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomps  
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991  
A: Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fami  
A: Reference number: A40956; MUID: 91271363  
A: Accession: B40956  
A: Molecule type: DNA  
A: Residues: 7-178 <EIS>  
A: Cross-references: GB:M63100; NID: g198389; PIDN: AAA39310.1; PID: g198390  
R: Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.  
Eur. J. Immunol. 21, 2775-2780, 1991  
A: Title: Cloning, heterologous expression and characterization of murine interleukin  
A: Reference number: A49031; MUID: 92037824  
A: Accession: A49031  
A: Molecule type: mRNA  
A: Residues: 23-178 <SHU>  
A: Cross-references: GB:S64082; NID: g238584; PIDN: AAB20265.1; PID: g238585  
A: Experimental source: peritoneal macrophages, ICR strain  
A: Note: sequence extracted from NCBI backbone (NCBI: 64082, NCBI: 64085)  
R: Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.  
J. Immunol. 146, 4228-4233, 1991  
A: Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene map  
A: Reference number: I56106; MUID: 91250712  
A: Accession: I56106  
A: Status: preliminary; translated from GB/EMBL/DBJ  
A: Molecule type: mRNA  
A: Residues: 1-178 <RES>  
A: Cross-references: GB:M74294; NID: g198387; PIDN: AAA39309.1; PID: g198388  
R: Zahedi, K.A.; Uhlar, C.M.; Prada, A.E.; Whitehead, A.S.  
Cytokine 6, 1-9, 1994  
A: Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regu  
A: Reference number: I52970; MUID: 94271931  
A: Accession: I52970  
A: Status: preliminary; translated from GB/EMBL/DBJ  
A: Molecule type: DNA  
A: Residues: 1-178 <RE2>  
A: Cross-references: GB: I32838; NID: g487864; PIDN: AAA20576.1; PID: g528978  
C: Genetics:



**QY** 15 IODINRVRVWVLDQTLLA-----VPRDRMSPTTIALISCRHVETLEKGRNPVIYLGI 67  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dd** 43 IDVNQRFTFLRNOLNAGVYQQGNWLKEIKIDVPDI-----EPHALLFI 88  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**QY** 68 NGNLNCLCAKVGGDPTLQLKEDIMLYNQPEPKVSFLFHSQSGRNSTESVAFFGW 137  
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dd** 89 HGKGKLCSVKSGDETRILQLAEVNIITDLSENRRKDKRFAFRSDSGPPTSESAACPGWF 148  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**QY** 128 IAVSSEGGCPILLTLQELGKANNTDFGL 154  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dd** 149 ICTAMEADQPVSILT-----NMPDEGV 169  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

**RESULT** 6  
S23010  
interleukin-1 beta precursor - sheep  
N;Alternate names: hematopoietin-1; IL-1 beta  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 08-Jun-1994 #sequence.revision 22-Nov-1996 #text\_change 15-Oct-1999  
C;Accession: S23010; #accession.SI3092; B61246  
R;Seow, H.F.; Rothenel, J.S.; David, M.J.; Wood, P.R.  
DNA Seq. L, 423-426, 1991  
A;Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.  
A;Reference number: S23010; MUID:92II19335  
A;Accession: S23010  
A:Molecule type: mRNA  
A;Residues: 1-266 <SEQ>  
A:Cross-references: EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809  
A>Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in F:Sargan, D.R.  
submitted to the EMBL Data Library, May 1992  
A;Reference number: S43047  
A;Accession: S43047  
A:Molecule type: mRNA  
A;Residues: 1-13,'C','15-54,'K','56-61,'S','63,'A','65-144,'L','146-266 <SAR>  
A:Cross-references: EMBL:X54796; NID:g1273; PIDN:CAA38566.1; PID:g1274  
R:Fiskerstrand, C.; Sargan, D.  
Nucleic Acids Res. 18, 7165, 1990  
A>Title: Nucleotide sequence of ovine interleukin-1 beta.  
A;Reference number: SI3092; MUID:91088326  
A;Accession: SI3092  
A:Molecule type: mRNA  
A;Residues: 1-13,'C','15-54,'K','56-61,'S','63,'A','65-144,'L','146-266 <FIS>  
A:Cross-references: EMBL:X54796  
A>Note: the authors translated the codon AGT for residue 62 as Arg R:Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.  
Immunology 74, 453-460, 1991  
A>Title: Molecular cloning and characterization of ovine IL-lalpha and IL-lbeta.  
A;Reference number: A61246; MUID:92120716  
A;Accession: B61246  
A:Molecule type: mRNA  
A;Residues: 1-144,'L','146-266 <AND>  
C;Comment: This protein lacks a conventional signal sequence for protein expression. The mature form of interleukin-1-beta, unlike interleukin 1-alpha, is inactive.  
C;Comment: Interleukin-1-beta precursor is less heavily myristoylated than C:Genetics:  
C;Gene: IL-1-beta  
C;Superfamily: interleukin-1  
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage activator protein-1  
F:114-266/Product: interleukin-1 beta #status predicted <MAT>



A:Residues: 1-267 <HUE>  
A:Cross-references: GB:M86725; NID:gl64607; PIDN:AAA02584.1; PID:gl64608  
A:Experimental source: alveolar macrophage  
C:Comment: This protein is a pleiotropic cytokine that mediates a variety of processes involved in the regulation of the immune response. Interleukin-1 beta is a precursor of interleukin-1 alpha, which is inactive.  
C:Comment: Interleukin-1 beta precursor is less heavily myristoylated than interleukin-1 alpha.  
C:Superfamily: interleukin-1  
C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage  
F:115-267/Product: Interleukin-1 beta #status predicted <Ill>  
F:77/Binding site: myristate (Iys) (covalent) #status predicted

Query Match 18.7%; Score 155; DB 1; Length 267;  
Best Local Similarity 22.8%; Pred. No. 8.3e-08;  
Matches 52; Conservative 34; Mismatches 66; Indels 76; Gaps 7;

QY 5 LKIDTPQSGTQ-DINHRVW---VLQDTLLIAPVRKDRMSPTV----- 43  
Db 39 LDLSLRNGSIQLQISHQLMNKSIRQMSVIVAVKPKNPSSQAFCDQDDQKSIFSIFF 98  
QY 44 ---IALISCR-----HVTLE----- 56  
Db 99 EPIILTCNDFFVCDANVQSMCKLQDKHSLVLAGPHMLKALHLLTGDLKRWFCM 158  
QY 57 -----KDRGN--PYILGLNGNLCLMCAKVGDDPTQLQKEKIMDLYNOPEPVKSFLFYH 109  
Db 159 SFVGDDSDNNKIPYTLGKGNLYLSCVMKNDPTTLQLEDID-PRYPRKDMKRFVYK 217  
QY 110 SOSGRNSTFESVAFPGFNIASFSGGCGPLLITQELGKANTDFGLTML 157  
Db 218 TEIKNRVFEFESALYPNWYISTQAEQKPVFLGNSKGRQDITFTWEVL 265

RESULT 11  
ICHLUB  
Interleukin-1 beta precursor [validated] - human  
N:Alternate names: hematopoietin-1; IL-1 beta  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1986 #sequence revision 15-May-1998 #text change 15-Sep-2000  
C:Accession: A25542; A29019; A94023; A93361; I51852; I65200; I38132; B27616; A01848; S19  
R:Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.  
Nucleic Acids Res. 14, 7897-7914, 1986  
A:Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev  
A:Reference number: A25542; MUID:87040762  
A:Accession: A25542  
A:Molecule type: DNA  
A:Residues: 1-5, 'K', 7-269 <CLA>  
A:Cross-references: GB:X04500; NID:g33788  
A:Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu  
R:Bensi, G.; Rauegi, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Mellii, M.  
Gene 52, 95-101, 1987  
A:Title: Human interleukin-1 beta gene.  
A:Reference number: A29019; MUID:87248099  
A:Accession: A29019  
A:Molecule type: DNA  
A:Residues: 1-269 <BR>  
A:Cross-references: GB:M15840; NID:gl86281; PIDN:AAA74137.1; PID:g336816  
R:Auron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinare  
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984  
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.  
A:Reference number: A94023; MUID:85088517  
A:Accession: A94023  
A:Molecule type: mRNA  
A:Residues: 1-5, 'K', 7-269 <AUR>  
A:Cross-references: GB:K02770; NID:gl86268; PIDN:AAA36106.1; PID:g307043  
R:March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S.  
Nature 315, 641-647, 1985  
A:Title: Cloning, sequence and expression of two distinct human interleukin-1 complement  
A:Reference number: A93361; MUID:85240547  
A:Accession: A93361  
A:Molecule type: mRNA  
A:Residues: 1-269 <MAR>

A:Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1; PID:g33790  
A:Note: parts of this sequence, including the amino end of the mature form, were conf  
R:Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.;  
Adv. Gene Technol. 22, 339-340, 1985  
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.  
A:Reference number: I51852  
A:Accession: I51852  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <WEB>  
A:Cross-references: GB:M54933; NID:gl86287; PIDN:AAA59136.1; PID:gl85288  
R:Nishida, T.; Nishino, M.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; H  
Biochem. Biophys. Res. Commun. 143, 345-352, 1987  
A:Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.  
A:Reference number: I52217; MUID:87156769  
A:Accession: I52200  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-269 <NIS>  
A:Cross-references: GB:M15330; NID:gl86283; PIDN:AAA59135.1; PID:g307045  
R:Kotenko, S.V.; Bulenkov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov  
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989  
A:Title: Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleu  
A:Reference number: I38131; MUID:90249285  
A:Accession: I38132  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-269 <KOT>  
A:Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663  
R:Zebo, K.M.; Wypych, J.; Tuschek, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley,  
Blood 71, 962-968, 1988  
A:Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoiet  
A:Reference number: A90732; MUID:88184226  
A:Accession: B27616  
A:Molecule type: protein  
A:Residues: 117-123, 'X', 125-126, 'X', 128 <ZSE>  
R:Stevenson, F.T.; Bursten, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.  
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993  
A:Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lys  
A:Reference number: A48293; MUID:93348250  
A:Contents: annotation; myristylation of lysines  
R:Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.  
Biochim. Biophys. Acta 1118, 25-35, 1991  
A:Title: The role of arginine residues in interleukin 1 receptor binding.  
A:Reference number: S19608; MUID:92110334  
A:Contents: annotation; type 1 IL-1 receptor interaction site  
A:Note: modification of Arg-120 by phenylglyoxal blocks receptor binding  
R:Clare, G.M.; Gronenborn, A.M.  
A:Reference number: A50049; PDB:611B  
A:Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269  
R:Clare, G.M.; Wingfield, P.T.; Gronenborn, A.M.  
Biochemistry 30, 2315-2323, 1991  
A:Title: High-resolution three-dimensional structure of interleukin 1beta in solution  
A:Reference number: A44675; MUID:91159409  
A:Contents: annotation; (1)H-NMR structural determination  
R:Hazuda, D.J.; Stricklet, J.; Simon, P.; Young, P.R.  
J. Biol. Chem. 266, 7081-7086, 1991  
A:Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a  
A:Reference number: A39774; MUID:91201363  
A:Contents: annotation  
R:Finzel, B.C.; Watenpaugh, K.D.; Einspahr, H.M.  
submitted to the Brookhaven Protein Data Bank, December 1989  
A:Reference number: A50016; PDB:111B  
A:Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269  
R:Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpaugh, K.D.; Einspa  
J. Mol. Biol. 209, 779-791, 1989  
A:Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom res  
A:Reference number: A44666; MUID:90064532  
A:Contents: annotation; X-ray crystallography, 2.0 angstroms  
C:Comment: This protein lacks a conventional signal sequence for protein export. Clea  
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.

C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a  
C;Genetics:  
A:Gene: GDB: IL1B  
A:Cross-references: GDB:120094; OMIM:147720  
A:Map position: 2q13-2q21  
A:Introns: 16/2; 33/3; 101/1; 156/1; 199/3  
C:Superfamily: Interleukin-1  
C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage  
F:117-269/Product: interleukin-1 beta #status experimental <IL1>  
F:76/Binding site: myristate (Lys) (covalent) (partial) #status experimental  
F:123/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 17.3%; Score 143.5; DB 1; Length 269;  
Best Local Similarity 34.5%; Pred. No. 1.2e-06;  
Matches 39; Conservative 15; Mismatches 56; Indels 3; Gaps 2;

Qy 46 LISCRHVETLEKDRGNPIYVLGNLCLMCAKVGDPQLQLEKIDMDLYNQPEPVKSF 105  
Db 157 VFSMSFVQGEESNDKIPVALGLKERNLYLSCLVKDKPTLOLESVDPKN-YPKKKMEKRF 215  
Qy 106 LFYHSQGRNSTESVAFPGWFIAVSSEGGCPILITQELGKANTYDFGLNMLF 150  
Db 216 VFNKIEINNKLEPESAQFPFNWYISTSQDENMPVFLGGTKGGQDITDF--TMQF 266

RESULT 12  
A30584  
Interleukin-1 beta precursor - rabbit  
N:Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating factor  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 25-May-1989 #sequence\_revision 22-Nov-1996 #text\_change 22-Jun-1999  
C:Accession: A27714; A30584; J00082; A32166  
R:Mori, S.; Goto, K.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.  
Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988  
A:Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiating factor  
A:Reference number: A27714; MUID:88134238  
A:Accession: A27714  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-268 <MOR>  
R:Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello, C.  
J. Immunol. 142, 2299-2306, 1989  
A:Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during  
A:Reference number: A30584; MUID:89176242  
A:Accession: A30584  
A:Molecule type: mRNA  
A:Residues: 1-268 <CAN>  
A:Cross-references: GB:M26295; NID:g516632; PIDN:AAA31373.1; PID:g516633  
R:Young, P.R.; Sylvester, D.  
Protein Eng. 2, 545-551, 1989  
A:Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and  
A:Reference number: A94230; MUID:89315718  
A:Accession: J00082  
A:Molecule type: mRNA  
A:Residues: 1-268 <YOU>  
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage  
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.  
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a  
C:Superfamily: Interleukin-1  
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen  
F:117-268/Product: interleukin-1 beta #status predicted <ILB>

Query Match 17.0%; Score 141.5; DB 1; Length 268;  
Best Local Similarity 33.0%; Pred. No. 1.8e-06;  
Matches 36; Conservative 16; Mismatches 56; Indels 1; Gaps 1;

Qy 46 LISCRHVETLEKDRGNPIYVLGNLCLMCAKVGDPQLQLEKIDMDLYNQPEPVKSF 105  
Db 156 VFSMSFVQGEESNDKIPVALGLRGNLYLSCLVKDKPTLOLESVD-PNRYPKKKMEKRF 214  
Qy 106 LFYHSQGRNSTESVAFPGWFIAVSSEGGCPILITQELGKANTYDFGL 154

Db 215 VFNKIEIKORLEPESAQFPFNWYISTSQTEYMPVFLGNNSGGQDLIDFSM 263

RESULT 13  
JC5646  
Interleukin-1 beta - horse  
C:Species: Equus caballus (domestic horse)  
C:Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 20-Jun-2000  
C:Accession: JC5646  
R:Kato, H.; Yoon, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa  
Gene 177, 11-16, 1996  
A:Title: Identification of an alternatively spliced transcript of equine interleukin-1  
A:Reference number: JC5646; MUID:97080493  
A:Accession: JC5646  
A:Molecule type: mRNA  
A:Residues: 1-214 <KAT>  
A:Cross-references: DDBJ:D42165; NID:g2463549; PIDN:BAA2528.1; PID:g2463550  
C:Comment: This protein mediates a variety of physiological response to infections and  
synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produ  
C:Superfamily: Interleukin-1

Query Match 16.6%; Score 137.5; DB 2; Length 214;  
Best Local Similarity 28.8%; Pred. No. 3.5e-06;  
Matches 44; Conservative 21; Mismatches 71; Indels 17; Gaps 3;

Qy 1 MEKAKITDPQSGIODINHRVWVLQDQTLIAVPRKDRMSPVTIALISC-RHVETLEKOR 59  
Db 71 VEKUKKIPVCSQAFQDDLR-----SLFSVFEVFCMSFVQGEETD 115  
Qy 60 GNPIYVLGNLCLMCAKVGDPQLQLEKIDMDLYNQPEPVKSFILFYHSQGRNSTFE 119  
Db 116 KIPVALGLKERNLYLSCLVKDKPTLOLETVD-PNTYPKKKMEKRFVFNKMEIKGNVEFE 174  
Qy 120 SVAPFGWFIAVSSEGGCPILITQELGKANTYDF 152  
Db 175 SAMYPNWIYSTSQAEKSPVFLGNTGRGRDITDF 207

RESULT 14  
I55969  
Interleukin-1 beta precursor - mouse  
N:Alternate names: hematopoietin-1; IL-1 beta  
C:Species: Mus musculus (house mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 22-Nov-1996 #text\_change 22-Jun-1999  
C:Accession: I55969; A24719; S13029  
R:Gray, P.W.; Glaister, D.; Chen, E.; Goeddel, D.V.; Pennica, D.  
J. Immunol. 137, 3644-3648, 1986  
A:Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for  
A:Reference number: I55969; MUID:87058957  
A:Accession: I55969  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-269 <RES>  
A:Cross-references: GB:M15131; NID:g198293; PIDN:AAA39276.1; PID:g309398  
R:Telford, J.L.; Macchia, G.; Massone, A.; Carlini, V.; Pallia, E.; Mellì, M.  
Nucleic Acids Res. 14, 9955-9963, 1986  
A:Title: The murine interleukin 1-beta gene: structure and evolution.  
A:Reference number: A24719; MUID:87117546  
A:Accession: A24719  
A:Molecule type: mRNA  
A:Residues: 1-269 <TEL>  
A:Cross-references: GB:X04964; NID:g52666; PIDN:CAA28637.1; PID:g52667  
R:Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McCall, A.S.; Geoghegan, K.F.; Otterness,  
FEBS Lett. 278, 98-102, 1991  
A:Title: Reduction of biological activity of murine recombinant interleukin-1beta by  
A:Reference number: S13029; MUID:91130610  
A:Accession: S13029  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 118-269 <DAU>  
C:Comment: This protein lacks a conventional signal sequence for protein export. Clea

Search completed: June 20, 2002, 15:03:52  
Job time: 162 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 20, 2002, 15:11:20 ; Search time 19.43 seconds  
(without alignments)  
314.858 Million cell updates/sec

Title: US-09-763-498-13

Perfect score: 830  
Sequence: 1 MEKALKIDTPQSGIQDINH.....ILTQELGKANTDFGLTMLF 158

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	195.5	23.6	178	1 IL1X_MOUSE	P25085 mus musculus
2	190.5	23.0	178	1 IL1X_RAT	P25086 rattus norv
3	186.5	22.5	177	1 IL1X_HORSE	O18999 equus caball
4	183.5	22.1	177	1 IL1X_HUMAN	P18510 homo sapien
5	178.5	21.5	177	1 IL1X_PIG	Q29056 sus scrofa
6	173.5	20.9	266	1 IL1B_SHEEP	P21621 ovis aries
7	172.5	20.8	174	1 IL1X_BOVIN	O77482 bos taurus
8	170.5	20.5	177	1 IL1X_RABIT	P26890 oryctolagus
9	167	20.1	266	1 IL1B_CEREAL	P51745 cervus elap
10	163.5	19.7	266	1 IL1B_BOVIN	P09428 bos taurus
11	162.5	19.6	266	1 IL1B_CAPHI	P79162 capra hircu
12	155	18.7	267	1 IL1B_PIG	P26889 sus scrofa
13	145.5	17.5	268	1 IL1B_MACFA	P79182 macaca fasc
14	145.5	17.5	269	1 IL1B_MACMU	P48090 macaca mula
15	143.5	17.3	269	1 IL1B_HUMAN	P01584 homo sapien
16	143.5	17.3	269	1 IL1B_MACNE	P51493 macaca neme
17	142.5	17.2	266	1 IL1B_CAVPO	O9wvg1 cavia porce
18	141.5	17.0	268	1 IL1B_RABIT	P14628 oryctolagus
19	137.5	16.6	269	1 IL1B_CERTO	P46648 cercocebus
20	133.5	16.1	268	1 IL1B_HORSE	Q28386 equus caball
21	128	15.4	268	1 IL1B_RAT	Q63264 rattus norv
22	126.5	15.2	267	1 IL1B_FELCA	P41687 felis silve
23	121	14.6	269	1 IL1B_MOUSE	P10749 mus musculus
24	118.5	14.3	269	1 IL1B_TRIVU	O9xs77 trichosurus
25	82	9.9	270	1 IL1A_HORSE	Q28385 equus caball
26	79	9.5	268	1 IL1A_CAPHI	P79161 capra hircu
27	79	9.5	270	1 IL1A_FELCA	O46613 felis silve
28	77	9.3	268	1 IL1A_BOVIN	P08831 bos taurus
29	76	9.2	501	1 GLPK_ECOLI	P08859 escherichia
30	75.5	9.1	270	1 IL1A_PIG	P18430 sus scrofa
31	75	9.0	1505	1 CUT2_HUMAN	O14529 homo sapien
32	74	8.9	268	1 IL1A_SHEEP	Q28579 ovis aries
33	73.5	8.9	1297	1 PUR4_HAEIN	P43847 haemophilus

34	72.5	8.7	325	1 RIR2_MYCLE	Q9cbq2 mycobacteri
35	72.5	8.7	950	1 IF2_IACLC	Q9x764 lactococcus
36	72	8.7	1220	1 IF2P_HUMAN	O60841 homo sapien
37	72	8.7	1955	1 PC15_HUMAN	Q96qui homo sapien
38	71.5	8.6	421	1 CHDE_MUCRO	P50325 mucor rouxi
39	71	8.6	872	1 MGR2_HUMAN	Q14416 homo sapien
40	71	8.6	1426	1 CUT2_MOUSE	P70298 mus musculus
41	71	8.6	1943	1 PC15_MOUSE	Q99p11 mus musculus
42	70.5	8.5	271	1 IL1A_MACFA	P79340 macaca fasc
43	70.5	8.5	556	1 CD19_HUMAN	P15391 homo sapien
44	70.5	8.5	944	1 IF2_LACIA	P58002 lactococcus
45	70	8.4	265	1 IL1A_CANFA	O46612 canis famil

## ALIGNMENTS

RESULT 1  
IL1X\_MOUSE  
ID IL1X\_MOUSE STANDARD; PRT; 178 AA.  
AC P25085; 070207;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)  
DE (IRAP).  
GN IL1RN OR IL-1RA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=91250712; PubMed=1828262;  
RA Zahedi K., Seldin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;  
RT "Mouse IL-1 receptor antagonist protein. Molecular characterization,  
RT gene mapping, and expression of mRNA in vitro and in vivo.";  
RL J. Immunol. 146:4228-4233(1991).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=91316273; PubMed=1830498;  
RA Matsushima H., Rousset M.F., Matsushima K., Hishinuma A., Sherr C.J.;  
RT "Cloning and expression of murine interleukin-1 receptor antagonist  
RT in macrophages stimulated by colony-stimulating factor 1.";  
RL Blood 78:616-623(1991).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC STRAIN=SWISS;  
RX MEDLINE=94271931; PubMed=8003626;  
RA Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;  
RT "The mouse interleukin 1 receptor antagonist protein: gene structure  
RT and regulation in vitro.";  
RL Cytokine 6:1-9(1994).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC STRAIN=FVB/DPA/1 LACJ;  
RX MEDLINE=98209757; PubMed=9550387;  
RA Gabay C., Porter B., Fantuzzi G., Arend W.P.;  
RT "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning  
RT and protein expression of intracellular isoform and tissue  
RT distribution of secreted and intracellular IL-1 receptor antagonist in  
RT vivo.";  
RL J. Immunol. 159:5905-5913(1997).  
RN [5]  
RP SEQUENCE OF 7-178 FROM N.A.  
RX MEDLINE=91271363; PubMed=1828896;  
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,  
RA Brandhuber B.J., Thompson R.C.;  
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1  
RT gene family: evolution of a cytokine control mechanism.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).  
RN [6]  
RP SEQUENCE OF 23-178 FROM N.A.

DE	Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE	(IRAP).
DE	IL1RN OR IL-1RA.
GN	Rattus norvegicus (Rat).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_taxID=10116;
CC	[1]
RN	SEQUENCE FROM N.A.
RP	MEDLINE=91271363; PubMed=1828896;
RP	Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA	Brandhuber B.J., Thompson R.C.;
RA	"Interleukin 1 receptor antagonist is a member of the interleukin 1
RT	gene family: evolution of a cytokine control mechanism.";
RT	Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RL	- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC	RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC	- !- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC	-----
CC	THIS SWISS-PROT entry is copyright. It is produced through a collabora-
CC	tion between the Swiss Institute of Bioinformatics and the EMBL outstat-
CC	ing European Bioinformatics Institute. There are no restrictions on
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
CC	EMBL; M63101; AAA41434.1; -
DR	PIR; C40956; C40956.
DR	HSP; P18510; IL1R.
DR	InterPro; IPR000975; Interleukin_1.
DR	Pfam; PF00340; IL1; 1.
DR	PRINTS; PR00264; INTERLEUKIN.
DR	ProDom; PD002536; Interleukin_1; 1.
DR	SMART; SM00125; IL1; 1.
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.
KW	Glycoprotein; Signal.
FT	SIGNAL 1 26
FT	CHAIN 27 178
FT	BY SIMILARITY.
FT	INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT	PROTEIN.
FT	DISULFID 92 142
FT	CARBOHYD 110 110
FT	SEQUENCE 178 AA; 20282 MW; F3A5754FB6C51B03 CRC64;
FT	(POTENTIAL).
FT	-----
QY	Query Match 23.0%; Score 190.5; DB 1; Length 178;
QY	Best local Similarity 35.1%; Pred. No. 7.5e-13;
QY	Matches 46; Conservative 20; Mismatches 50; Indels 15; Gaps
QY	15 IQDINHRWVLQDOTLIA-----VPRKDRSPVTIALISCRHVFLEKDRGNPIYLGLNGL 70
QY	41 IWDNQKTFYLRNNLIAGYLQGPNTKLEKIDMVPIDFRNV-----FLIHGG 89
QY	71 NLCILMCAKVGDPQTLQLEKIDIMLYNQPEPVKSLFYVHSGSGRNSFTESVAPPGWFI 130
QY	90 KLCISCVKSGDDTKLQLEEVNITDLNKKNEEDKRFTRFIRSETGTTSFSLACPGWFLCT 149
QY	131 SSEGGCPLILT 141
QY	150 TLEADHPVSLT 160
QY	-----
QY	RESULT 3
QY	IL1X_HORSE
QY	IL1X_HORSE STANDARD; PRT; 177 AA.
QY	IC AD Q18999; 077745;
QY	15-DEC-1998 (Rel. 37, Created)
QY	15-DEC-1998 (Rel. 37, Last sequence update)
QY	15-JUL-1999 (Rel. 38, Last annotation update)
QY	Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
QY	(IRAP).
QY	IL1RN OR IL1RA.
QY	Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=97366446; PubMed=9223227;  
 RA Kato H., Ohashi T., Matsushiro H., Watari T., Goitsuka R.,  
 RA Tsujimoto H., Hasegawa A.;  
 RT "Molecular cloning and functional expression of equine Interleukin-1  
 RT receptor antagonist.";  
 RL Vet. Immunol. Immunopathol. 56:221-231(1997).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=98285942; PubMed=9622739;  
 RA Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;  
 RT "Cloning of equine interleukin-1 receptor antagonist and  
 RT determination of its full-length cDNA sequence.";  
 RL Am. J. Vet. Res. 59:712-716(1998).  
 CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS  
 CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.  
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: D83714; BAA22529.1; -;  
 DR EMBL: U92482; AAC39257.1; -;  
 DR HSP: P18510; IL1R.  
 DR InterPro: IPR000975; Interleukin\_1.  
 DR Pfam: PF00340; IL1; 1.  
 DR PRINTS: PRO0264; INTERLEUKIN\_1.  
 DR PRODOM: PRO02536; Interleukin\_1; 1.  
 DR SMART: SM00125; IL1; 1.  
 DR PROSITE: PS00253; INTERLEUKIN\_1; 1.  
 KW Glycoprotein; Signal.  
 FT SIGNAL 1 25 BY SIMILARITY.  
 FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST  
 FT PROTEIN.  
 FT DISULFID 91 141 BY SIMILARITY.  
 FT CARBOHYD 109 109 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CONFLICT 19 19 F -> L (IN REF. 2).  
 SQ SEQUENCE 177 AA; 20459 MW; 1ABC377F1FCF60B CRC64;  
 Query Match 22.58; Score 186.5; DB 1; Length 177;  
 Best Local Similarity 33.38; Pred. No. 2e-12;  
 Matches 43; Conservative 25; Mismatches 54; Indels 7; Gaps 2;  
 QY 15 IODINRHWVLDQDTLIAVPRKDRMSPTVIALISCRHVEPLEKDRGNPIYVLGNGINLCL 74  
 Db 40 IWDVNOKTYMRNOLVAGYQESNTKLOEKI----DVVPIEDP---ALFLGLHGRKCLCL 92  
 QY 75 MCACVKDQDTLQLEKEDIMLYNOPEVPKSLFVHSGSGNSTFESVAPGFHFIASVSG 134  
 Db 93 ACVKSDEIRFOLEAVNITDLSKNEKNKRTFIRNSGTTTSFSAACPGWFLCTAQEA 152  
 QY 135 GCPILITQEQ 143  
 Db 153 DRPVSLTNK 161  
 RESULT 4  
 IL1X\_HUMAN STANDARD; PRT; 177 AA.  
 AC P18510; Q9UPC0;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (ICIL-  
 DE 1RA) (IRAP) (IL-1RN).  
 GN IL1RN OR IL1RA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=90220867; PubMed=2139180;  
 RA Carter D.B., Deibel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,  
 RA Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N.,  
 RA Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Sieu L.C.,  
 RA Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinrikson R.L.,  
 RA Truesdell S.E., Shelly J.A., Eessalu T.E., Taylor B.M., Tracey D.E.;  
 RT "Purification, cloning, expression and biological characterization of  
 RT an interleukin-1 receptor antagonist protein.";  
 RL Nature 344:633-638(1990).  
 RN [2]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=90136921; PubMed=2137201;  
 RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,  
 RA Hannum C.H., Thompson R.C.;  
 RT "Primary structure and functional expression from complementary DNA  
 RT of a human interleukin-1 receptor antagonist.";  
 RL Nature 343:341-346(1990).  
 RN [3]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=91271363; PubMed=1828896;  
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,  
 RA Brandhuber B.J., Thompson R.C.;  
 RT "Interleukin 1 receptor antagonist is a member of the interleukin 1  
 RT gene family: evolution of a cytokine control mechanism.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).  
 RN [4]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=92338323; PubMed=1385987;  
 RA Lennard A., Gorman P., Carrier M., Griffiths S., Scotney H.,  
 RA Sheer D., Solari R.;  
 RT "Cloning and chromosome mapping of the human interleukin-1 receptor  
 RT antagonist gene.";  
 RL Cytokine 4:83-89(1992).  
 RN [5]  
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).  
 RX MEDLINE=97146044; PubMed=892991;  
 RA Jenkins J.K., Drong R.P., Shuck M.E., Bienkowski M.J., Slightom J.L.,  
 RA Arend W.P., Smith M.F. Jr.;  
 RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific  
 RT and inducible regulatory regions.";  
 RL J. Immunol. 158:748-755(1997).  
 RN [6]  
 RN SEQUENCE FROM N.A. (ISOFORM 2).  
 RX MEDLINE=91219436; PubMed=1827201;  
 RA Haskill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,  
 RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;  
 RT "cDNA cloning of an intracellular form of the human interleukin 1  
 RT receptor antagonist associated with epithelium.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).  
 RN [7]  
 RN SEQUENCE FROM N.A. (ISOFORM 3).  
 RX MEDLINE=95355865; PubMed=7629520;  
 RA Muzio M., Polentarutti N., Sironi M., Poli G., De Gioia L.,  
 RA Introna M., Mantovani A., Colotta F.;  
 RT "Cloning and characterization of a new isoform of the interleukin 1  
 RT receptor antagonist.";  
 RL J. Exp. Med. 182:623-628(1995).  
 RN [8]  
 RN SEQUENCE OF 26-45.  
 RX MEDLINE=90136920; PubMed=2137200;  
 RA Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J.,  
 RA Heimdal P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;  
 RT "Interleukin-1 receptor antagonist activity of a human interleukin-1  
 RT inhibitor.";





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QY 122 APPGWFIASVSGGCPILILQELGKANTWDTGLTML 157
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 229 LYPNNYISTQIEKPVFLGRFRGGQDITDFRMETL 264

RESULT 7
IL1X_BOVIN STANDARD; PRT; 174 AA.
AC 077482;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98305607; PubMed=9643454;
RA Kirisawa R., Fukuda T., Yamanaka H., Hagiwara K., Goto M., Obata Y.,
RA Yoshino T., Iwai H.;
RT "Enzymatic amplification and expression of bovine interleukin-1
RT receptor antagonist cDNA."
RL Vet. Immunol. Immunopathol. 62:197-208(1998).
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC
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CC -----
CC EMBL; AB005148; BAA31854.1; -
CC HSSP; P18510; IL1R.
CC InterPro; IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC PRINTS; PR00264; INTERLEUKIN1.
CC ProDom; PD002536; Interleukin_1; 1.
CC SMART; SM00125; IL1; 1.
CC PROSITE; PS00253; INTERLEUKIN_1; 1.
CC Glycoprotein; Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 174 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT FT
FT FT
FT DISULFID 89 139 BY SIMILARITY.
FT CARBOHYD 107 107 N-LINKED (GLCNAC... ) (POTENTIAL).
FT SEQUENCE 174 AA; 19926 MW; 1E56E7F224FF851F CRC64;
Query Match 20.8%; Score 172.5; DB 1; Length 174;
Best Local Similarity 30.6%; Pred. No. 5.6e-11;
Matches 41; Conservative 25; Mismatches 47; Indels 21; Gaps 2;
QY 15 IODINHRVWLODQTLTA-----VPRKDRNSPVNIALISCRHVETLEKGRNPYIGL 67
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 38 IWDVWQKIFYLRNQLVAGYQGNPKLEKIDVFI-----EPHTMFUGI 83
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 68 NGLNLCMLCAKVGDOPTLQLEKIDMDLYNQPEPKVSFLFYHSQSGRNSTFESVAFPGWF 127
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 84 HGGKLCACVKRSGDEIKLKLEAVNITDNLQNREQDKRFAFIRFDNGPTTSFESAACPGWF 143
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 128 IAVSSEGGCPILIT 141
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 144 LCTSLADQPGVLT 157
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
```

```
RESULT 8
IL1X_RABIT STANDARD; PRT; 177 AA.
AC P26890;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL1RA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94165101; PubMed=7509813;
RA Cominelli F., Bortolami M., Pizarro T.T., Monsacchi L., Ferretti M.,
RA Brewer M.T., Eisenberg S.P., Ng R.K.;
RT "Rabbit interleukin-1 receptor antagonist. Cloning, expression,
RT functional characterization, and regulation during intestinal
RT inflammation."
RL J. Biol. Chem. 269:6962-6971(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Hamada H., Mulligan R.C.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93052512; PubMed=1427977;
RA Goto F., Goto K., Miyata T., Ohkawara S., Takao T., Mori S.,
RA Furukawa S., Maeda T., Iwanaga S., Shimonishi Y., Yoshinaga M.;
RT "Interleukin-1 receptor antagonist in inflammatory exudate cells of
RT rabbits. Production, purification and determination of primary
RT structure."
RL Immunology 77:235-244(1992).
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC
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CC -----
CC EMBL; S68977; AAB30093.1; -
CC EMBL; M57526; AAA31374.1; -
CC EMBL; D21832; BAA04860.1; -
CC PIR; A54377; A54377.
CC HSSP; P18510; IL1R.
CC InterPro; IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC PRINTS; PR00264; INTERLEUKIN1.
CC ProDom; PD002536; Interleukin_1; 1.
CC SMART; SM00125; IL1; 1.
CC PROSITE; PS00253; INTERLEUKIN_1; 1.
CC Glycoprotein; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT FT
FT DISULFID 91 141 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC... ) (POTENTIAL).
FT SEQUENCE 177 AA; 20214 MW; F5BC087F097FEAF CRC64;
Query Match 20.5%; Score 170.5; DB 1; Length 177;
Best Local Similarity 30.6%; Pred. No. 9.3e-11;
Matches 44; Conservative 21; Mismatches 52; Indels 27; Gaps 3;
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[illegible]

## RESULT

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ID      IL1B_CEREL      STANDARD;      PRT;      266 AA.
AC      P51745;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Interleukin-1 beta precursor (IL-1 beta).
DE      IL1B.
GN      Cervus elaphus (Red deer).
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoides;
OC      Cervidae; Cervinae; Cervus.
OX      NCBI_TaxId=9860;
RN      [1]
RS      SEQUENCE FROM N.A.
RL      Lockhart E.A.;
RL      Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC      THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC      MATURATION AND PROLIFERATION, AND FIBROBLAST GROWTH FACTOR
CC      ACTIVITY. IL-1S ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC      IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC      THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC      (BY SIMILARITY).
CC      -!- SUBUNIT: MONOMER (By similarity).
CC      -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC      AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC      -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC      PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC      OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC      SECRETORY PROTEINS (By similarity).
CC      -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC      -----
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DR	EMBL; U20500; AAA62234.1; -.	
DR	HSP; P01564; IHIB.	
DR	InterPro; IPR002348; IL1_HBGF.	
DR	InterPro; IPR000975; Interleukin_1.	
DR	InterPro; IPR003502; Interleukin_1_prop.	
DR	Pfam; PF00340; IL1; 1.	
DR	Pfam; PF02394; IL1_propep; 1.	
DR	PRINTS; PR00262; IL1HBGF.	
DR	ProDom; PD002536; Interleukin_1; 1.	
DR	SMART; SM00125; IL1; 1.	
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.	
KW	Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.	
FT	PROPEP	1
FT		113
FT		BY SIMILARITY.
FT	CHAIN	114 266
FT	SEQUENCE	266 AA; 30529 MW; 4F40B4E6FD09F060 CRC64;
FT		

Query Match 20.18; Score 167; DB 1; Length 266;

[illegible]

RESULT 10

IL1B_BOVIN	STANDARD;	PRT;	266 AA.
ID	IL1B_BOVIN		
DC	P09428;		
DT	01-MAR-1989 (Rel. 10, Created)		
DT	01-MAR-1989 (Rel. 10, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	Interleukin-1 beta precursor (IL-1 beta).		
DE	IL1B,		
GN	Bos taurus (Bovine).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
ON	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89016591; PubMed=3262866;		
RA	Leong S.R., Flagg G.M., Lawman M., Gray P.W.;		
RT	"The nucleotide sequence for the cDNA of bovine interleukin-1 beta."		
RL	Nucleic Acids Res. 16:9054-9054(1988).		

```

SEQUENCE FROM N.A.
MEDLINE=88318652; PubMed=3261832;
Malliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D.,
Gillis S., Cerretti D.P.;
"Cloning, sequence and expression of bovine interleukin 1 alpha and
interleukin 1 beta complementary DNAs.";
Mol. Immunol. 25:429-437(1988).
-!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
TUMORCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYOGENS, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVIAL CELLS.
-!- SUBUNIT: MONOMER.
-!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
-!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
SECRETORY PROTEINS.
-!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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EMBL; M35589; AAA30585.1; -
EMBL; X12498; CAA31018.1; -
EMBL; M37211; AAA30584.1; -
PIR; J10010; ICB01B.
PIR; S01380; S01380.
HSP; P01584; 1H1B.

```

```
DR InterPro: IPR002348; IL1_HBGF.
DR InterPro: IPR000975; Interleukin_1.
DR InterPro: IPR003502; Interleukin_1_prop.
DR Pfam: PF00340; IL1; 1.
DR Pfam: PF02394; IL1_HBGF.
DR PRINTS: PR00262; Interleukin_1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR SMART: PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 113
FT CHAIN 114 266 INTERLEUKIN-1 BETA.
FT CONFLICT 252 252 A -> G (IN REF. 2).
SQ SEQUENCE 266 AA; 30774 MW; 9D1EF8F575070586 CRC64;

Query Match 19.7%; Score 163.5; DB 1; Length 266;
Best Local Similarity 36.8%; Pred. No. 8.3e-10;
Matches 39; Conservative 16; Mismatches 50; Indels 1; Gaps 1;

QY 52 VETLEKDRGNPIYGLNGLCLMCAKVGDOPTLQKKEKIDMDLYNOPEPVKSLFYHSQ 111
DB 160 VQGEEDNKIPALGDKKNLYLSCVKKGDPTLQLEEVDPKVYPRKRNMEKREVFYKTE 218
QY 112 SGRNSTFESVAPFGWFIAYVSGGCPPLILTQELGKANTTDFGLTML 157
DB 219 IKNTVFESVLPYNNWYSTSQIEERPVLFGHFRAGQDITDFRMETL 264

RESULT 11
IL1B_CAPHI
ID IL1B_CAPHI STANDARD; PRT; 266 AA.
AC P79162;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Takakura H., Hashimoto O., Mori Y., Tatsumi M.;
RT "Molecular cloning and expression of caprine IL-1alpha and
RT IL-1beta";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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DR EMBL: D63351; BAA09675.1; -.
DR HSSP: P01584; IHIB.
DR InterPro: IPR002348; IL1_HBGF.
DR InterPro: IPR000975; Interleukin_1.
DR InterPro: IPR003502; Interleukin_1_prop.
DR Pfam: PF00340; IL1; 1.
DR Pfam: PF02394; IL1_HBGF.
DR PRINTS: PR00262; Interleukin_1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR SMART: PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 113 BY SIMILARITY.
FT CHAIN 114 266 INTERLEUKIN-1 BETA.
SQ SEQUENCE 266 AA; 30769 MW; 59F7B39BD1D4DDA5 CRC64;

Query Match 19.6%; Score 162.5; DB 1; Length 266;
Best Local Similarity 31.4%; Pred. No. 1.1e-09;
Matches 49; Conservative 25; Mismatches 63; Indels 19; Gaps 4;

QY 2 EKALKIDTPQSGIQDINHVRVWVLDQDTLQKKEKIDMDLYNOPEPVKSLFYHSQSRNSTFESV 121
DB 128 QKSLVLDSP-----CVLKALHLLS-----QEMSREVFVCMSS--FVQGEERDNKI 169
QY 62 PIVLGLNGLCLMCAKVGDOPTLQKKEKIDMDLYNOPEPVKSLFYHSQSRNSTFESV 121
DB 170 PVALGIRDKNLYLSCVKKGDPTLQLEEVDPKVYPRKRNMEKREVFYKTEIKNTVFESV 228
QY 122 APFGWFIAYVSGGCPPLILTQELGKANTTDFGLTML 157
DB 229 LYPNNWYSTSQIEERPVLFGHFRAGQDITDFRMETL 264

RESULT 12
IL1B_PIG
ID IL1B_PIG STANDARD; PRT; 267 AA.
AC P26889;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN IL1B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93314975; PubMed=8325511;
RA Huebner M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.;
RT "Cloning, sequencing, and regulation of an mRNA encoding porcine
RT interleukin-1 beta.";
RL Gene 129:285-289(1993).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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DR EMBL; M86725; AAA02584.1; -.  
DR PIR; JN0724; JN0724.  
DR HSSP; P01584; 1H1B.  
DR InterPro; IPR002348; IL1\_HBGF.  
DR InterPro; IPR000975; Interleukin\_1.  
DR InterPro; IPR003502; Interleukin\_1\_prop.  
DR Pfam; PF00340; IL1; 1.  
DR Pfam; PF02394; IL1\_propep; 1.  
DR PRINTS; PR00262; IL1HBGF.  
DR ProDom; PD002536; Interleukin\_1; 1.  
DR SMART; SM00125; IL1; 1.  
DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.  
FT PROPEP 1 114 BY SIMILARITY.  
FT CHAIN 115 267 INTERLEUKIN-1 BETA.  
SQ SEQUENCE 267 AA; 30404 MW; 7F6B92B784D5086F CRC64;

Query Match 18.7%; Score 155; DB 1; Length 267;  
Best Local Similarity 22.8%; Pred. No. 6.5e-09;  
Matches 52; Conservative 34; Mismatches 66; Indels 76; Gaps 7;  
QY 5 LKIDTPQSGSIQ-DINHRVW---VLQDTLLIAPVRKDRMSPTV----- 43  
Db 39 LDGLSLRNGSIQLQISHOLMKNKSIRQMVSIVAVKPKMNPSSQAFCDDDQKSIIFSIFE 98  
QY 44 ---IALISCR-----HVETLE----- 56  
Db 99 EEPILLETNCDDFVCDANVSMECKLQDKHKSIVLAGPHMLKALHLLTGDLKREVVFWM 158  
QY 57 -----KDRGN---PIYGLGNGNLCLMCAKVGDDPTQLQKEKDIMLYNQPEPVKSLFYH 109  
Db 159 SFVGGDDSNKIPVTIGIKNNLYLSCVMKDNTPTLQLEDID-PKRYPKRDMKREVFYK 217  
QY 110 SOSGRNSTFESVAPPGFIAVSSEGGCPILITQELGKANTTDFGLTMLF 157  
Db 218 TEIKNRVEFSALPNWYISTSQAEQKPVFLGNSKGRQDITDFTMEVL 265

RESULT 13  
IL1B\_MACFA STANDARD; PRT; 268 AA.  
AC P79182;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Interleukin-1 beta precursor (IL-1 beta).  
GN IL1B.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Thymus;  
RA Totsuka K., Takakura H., Hashimoto O., Tatsumi M.;  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
CC -!- SUBUNIT: MONOMER.  
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS

CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
CC SECRETORY PROTEINS.  
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
CC -----

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CC -----

DR EMBL; D63353; BAA09677.1; -.  
DR HSSP; P01584; 1H1B.  
DR InterPro; IPR002348; IL1\_HBGF.  
DR InterPro; IPR000975; Interleukin\_1.  
DR InterPro; IPR003502; Interleukin\_1\_prop.  
DR Pfam; PF00340; IL1; 1.  
DR Pfam; PF02394; IL1\_propep; 1.  
DR PRINTS; PR00262; IL1HBGF.  
DR ProDom; PD002536; Interleukin\_1; 1.  
DR SMART; SM00125; IL1; 1.  
DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.  
FT PROPEP 1 116 BY SIMILARITY.  
FT CHAIN 117 268 INTERLEUKIN-1 BETA.  
SQ SEQUENCE 268 AA; 30425 MW; CFB7266E3E2C05B4 CRC64;

Query Match 17.5%; Score 145.5; DB 1; Length 268;  
Best Local Similarity 34.5%; Pred. No. 6.4e-08;  
Matches 39; Conservative 15; Mismatches 56; Indels 3; Gaps 2;  
QY 46 LJSCHRVETLEKDRGNPIYGLGNGNLCLMCAKVGDDPTQLQKEKDIMLYNQPEPVKSF 105  
Db 157 VFSSMFSQVEESNDKIPVALGKAKNLYLSCVLKDDKPTQLQESVDPKN-YPKKMKRFR 215  
QY 106 LFYHSGSNGNSTFESVAPPGFIAVSSEGGCPILITQELGKANTTDFGLTMLF 158  
Db 216 VENKINKEFESAQFPNWIYSTSQAESEMPVFLGGTRGGQDITDF--TMQF 266  
RESULT 14  
IL1B\_MACMU STANDARD; PRT; 269 AA.  
AC P48090;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Interleukin-1 beta precursor (IL-1 beta).  
GN IL1B.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;  
RL Medline=96003435; PubMed=7561102;  
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
CC -!- SUBUNIT: MONOMER.  
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

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CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U19845; AAA86709.1; -
DR HSSP: P01584; LHIB
DR InterPro: IPR002348; IL1_HBGF
DR InterPro: IPR000975; Interleukin_1.
DR InterPro: IPR003502; Interleukin_1_prop.
DR Pfam: PF00340; IL1; 1.
DR PRINTS: PR002394; IL1_propep; 1.
DR ProDom: PD002336; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 116 BY SIMILARITY.
FT CHAIN 117 269 INTERLEUKIN-1 BETA.
SQ SEQUENCE 269 AA; 30481 MW; A7CD59EBAC120EC7 CRC64;

Query Match 17.5%; Score 145.5; DB 1; Length 269;
Best Local Similarity 34.5%; Pred. No. 6.5e-08;
Matches 39; Conservative 15; Mismatches 56; Indels 3; Gaps 2;

QY 46 LISCRHVETLEKDRGNPIYGLNGLNLCMAKVGDPQLQLKEKDIMPYLNQPEPVKSF 105
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 157 VFSMSFVQGEESDKIPVALGKAKNLYLSCLVKDDKPTQLQESVDPKN-YPKKKMEKRF 215
QY 106 LFVHSGSRNSTPESVAFQGWFTAVSSEGGCPILITQELGKANTDTDFGLTMLF 158
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 216 VFKNKIEINKLEFESAQFPNWIYSTQAEKNMPVFLGGTRGGQDITDF--TMOF 266

RESULT 15
IL1B_HUMAN
ID IL1B_HUMAN STANDARD; PRT; 269 AA.
AC P01584; Q96HE5; Q9UCF6;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta) (Catabolin).
GN IL1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85088517; PubMed=6093565;
RA Auron P.E., Webb A.C., Rosenwasser L.J., Mucci S.F., Rich A.,
RA Wolff S.M., Dinarello C.A.;
RT "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:7907-7911(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85240547; PubMed=2989698;
RA March C.J., Mosley B., Larsen A., Cerretti D.P., Braedt G., Price V.,
RA Gillis S., Henney C.S., Kronheim S.R., Grabstein K., Conlon P.J.,
RA Hopp T.P., Cosman D.;
RT "Cloning, sequence and expression of two distinct human interleukin-1
RT complementary DNAs.";
RL Nature 315:641-647(1985).

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RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87040762; PubMed=3490654;
RA Clark B.D., Collins K.L., Gandy M.S., Webb A.C., Auron P.E.;
RT "Genomic sequence for human prointerleukin 1 beta: possible evolution
RT from a reverse transcribed prointerleukin 1 alpha gene.";
RL Nucleic Acids Res. 14:7897-7914(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248099; PubMed=2954882;
RA Bensi G., Raugel G., Falla E., Carinci V., Buonamassa D.T., Melli M.;
RT "Human interleukin-1 beta gene.";
RL Gene 52:95-101(1987).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=90249285; PubMed=2635664;
RA Kotenko S.V., Buletkov M.T., Velko V.P., Epishin S.M., Lomakin I.B.,
RA Emel'yanov A.V., Kozlov A.P., Konusova V.G., Kotov A.Y.,
RA Kurbatova T.V., Reshetnikov V.L., Simbirtsev A.S., Ketlinskii S.A.,
RA Vinetskii Y.P.;
RT "Cloning of the cDNA coding for human prointerleukin-1 alpha and
RT prointerleukin-1 beta.";
RL Dokl. Akad. Nauk SSSR 309:1005-1008(1989).
RN [6]
RP SEQUENCE FROM N.A.
RX Webb A.C., Dinarello C.A., Rosenwasser L.J., Mucci S.F., Rich A.,
RA Wolff S.M., Auron P.E.;
RT "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";
RL Adv. Gene Technol. 22:339-340(1985).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=87156769; PubMed=3493774;
RA Nishida T., Nishino N., Takano M., Kawai K., Bando K., Masui Y.,
RA Nakai S., Hirai Y.;
RT "cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell
RT line.";
RL Biochem. Biophys. Res. Commun. 143:345-352(1987).
RN [8]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE OF 117-128.
RX MEDLINE=88184226; PubMed=3281727;
RA Zsebo K.M., Wypych J., Yuschekoff V.N., Lu H., Hunt P., Dukes P.P.,
RA Langley K.E.;
RT "Effects of hematopoietin-1 and interleukin 1 activities on early
RT hematopoietic cells of the bone marrow.";
RL Blood 71:962-968(1988).
RN [10]
RP SEQUENCE OF 114-135.
RX TISSUE=Skin;
RA MEDLINE=92013781; PubMed=1919436;
RA Mizutani H., Schechter N., Lazarus G., Black R.A., Kupper T.S.;
RT "Rapid and specific conversion of precursor interleukin 1 beta (IL-1
RT beta) to an active IL-1 species by human mast cell chymase.";
RL J. Exp. Med. 174:821-825(1991).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=88211543; PubMed=3259176;
RA Priestle J.P., Schar H.-P., Grutter M.G.;
RT "Crystal structure of the cytokine interleukin-1 beta.";
RL EMBO J. 7:339-343(1988).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=9009325; PubMed=2602367;
RA Priestle J.P., Schar H.-P., Grutter M.G.;
RT "Crystallographic refinement of interleukin 1 beta at 2.0-A
RT resolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9667-9671(1989).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

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RX MEDLINE=90064532; PubMed=2585509;  
 RA Finzel B.C., Clancy L.L., Holland D.R., Muchmore S.W.,  
 RA Watenpaugh K.D., Einspahr H.M.;  
 RT "Crystal structure of recombinant human interleukin-1 beta at 2.0-A  
 RT resolution.";   
 RL J. Mol. Biol. 209:779-791(1989).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH RECEPTOR.  
 RX MEDLINE=97215903; PubMed=9062193;  
 RA Vigers G.P., Anderson L.J., Caffes P., Brandhuber B.J.;  
 RT "Crystal structure of the type-I interleukin-1 receptor complexed  
 RT with interleukin-1beta.";   
 RL Nature 386:190-194(1997).  
 RN [15]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=90321925; PubMed=2372550;  
 RA Driscoll P.C., Gronenborn A.M., Wingfield P.T., Clore G.M.;  
 RT "Determination of the secondary structure and molecular topology of  
 RT interleukin-1 beta by use of two- and three-dimensional heteronuclear  
 RT 15N-1H NMR spectroscopy.";   
 RL Biochemistry 29:4668-4682(1990).  
 RN [16]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=91159409; PubMed=2001363;  
 RA Clore G.M., Wingfield P.T., Gronenborn A.M.;  
 RT "High-resolution three-dimensional structure of interleukin 1 beta in  
 RT solution by three- and four-dimensional nuclear magnetic resonance  
 RT spectroscopy.";   
 RL Biochemistry 30:2315-2323(1991).  
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
 CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS  
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
 CC SECRETORY PROTEINS.  
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
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 CC -----  
 DR EMBL; M15840; AAA74137.1; -;  
 DR EMBL; X02532; CAA26372.1; -;  
 DR EMBL; K02770; AAA36106.1; -;  
 DR EMBL; X04500; CAA28185.1; -;  
 DR EMBL; X56087; CAA39567.1; -;  
 DR EMBL; M54933; AAA59136.1; -;  
 DR EMBL; M15330; AAA59135.1; -;  
 DR EMBL; BC008678; AAR08678.1; -;  
 DR PIR; A01848; ICHU1B.  
 DR PIR; A25542; A25542.  
 DR PIR; A29019; A29019.  
 DR PIR; B27616; B27616.  
 DR PIR; S19626; S19626.  
 DR PDB; 111B; 15-OCT-92.  
 DR PDB; 211B; 15-JUL-93.  
 DR PDB; 411B; 15-JAN-93.  
 DR PDB; 511B; 15-OCT-94.  
 DR PDB; 611B; 15-OCT-92.  
 DR PDB; 711B; 15-OCT-92.  
 DR PDB; 21B1; 15-APR-92.  
 DR PDB; 31B1; 15-APR-92.

DR PDB; 41B1; 15-JUL-92.  
 DR PDB; 1H1B; 31-JAN-94.  
 DR PDB; 110B; 17-AUG-96.  
 DR PDB; 111B; 04-FEB-98.  
 DR PDB; 91B; 06-JAN-99.  
 DR MIM; 147720; -;  
 DR InterPro; IPR002348; IL1\_HBGF.  
 DR InterPro; IPR00975; Interleukin\_1.  
 DR InterPro; IPR003502; Interleukin\_1\_prop.  
 DR Pfam; PF00340; IL1; 1  
 DR Pfam; PF02394; IL1\_propep; 1.  
 DR PRINTS; PR00262; IL1HBGF.  
 DR ProDom; PD002536; Interleukin\_1; 1.  
 DR SMART; SM00125; IL1; 1.  
 DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
 KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;  
 KW 3D-structure.  
 FT PROPEP 1 116 INTERLEUKIN-1 BETA.  
 FT CHAIN 117 269 K -> E (IN REF. 2, 6 AND 8).  
 FT CONFLICT 6 6 D -> H (IN REF. 7).  
 FT CONFLICT 20 20 E -> Q (IN REF. 7).  
 FT CONFLICT 111 111 E -> A (IN REF. 7).  
 FT CONFLICT 177 177 G -> P (IN REF. 7).  
 FT CONFLICT 214 214 R -> P (IN REF. 7).  
 FT STRAND 121 128  
 FT TURN 129 130  
 FT STRAND 132 138  
 Query Match 17.3%; Score 143.5; DB 1; Length 269;  
 Best Local Similarity 34.5%; Pred. No. 1e-07;  
 Matches 39; Conservative 15; Mismatches 56; Indels 3; Gaps 2;  
 Qy 46 LISCRHVETLEKDRGNIYGLNGLNCLMCAKVGQDPTQLQKEKIMDLYNQPEPKSF 105  
 Db 157 VFMSFVQGEESNDKIPVALGLKEKNLYLSVLCVLDKDDKPTQLQLESVDPKN-YPKKMKRF 215  
 Qy 106 LFYHSQSGRNSTFESVAFPGWFIASVSESGCPLILTQELGKANTTDFGLTMLF 158  
 Db 216 VFNKIEINNKLEFESAQFPNNWYISTSOAENMPVFLGGTKGGQDITDF--TMOF 266

Search completed: June 20, 2002, 15:11:20  
 Job time: 445 sec

us-09-763-498-13.rsp

Fri Jun 21 14:40:28 2002

...

GenCore version 4.5  
 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:10:54 ; Search time 61.16 Seconds  
 (without alignments)  
 446.913 Million cell updates/sec

Title: us-09-763-498-13  
 Perfect score: 830  
 Sequence: 1 MEKALKIDTPQSGSIQDINH.....ILTQELGKANTDFGLTMLF 158

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SPTREMBL19:\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	826	99.5	158	4	Q9UHA7	Q9UHA7 homo sapien
2	466.5	56.2	169	4	Q9NZH8	Q9NZH8 homo sapien
3	463	55.8	160	11	Q9JLA2	Q9JLA2 mus musculus
4	384	46.3	157	4	Q9UHA5	Q9UHA5 homo sapien
5	333	40.1	183	11	Q9D6Z6	Q9D6Z6 mus musculus
6	210	25.3	192	4	Q9UHA6	Q9UHA6 homo sapien
7	210	25.3	218	4	Q9NZH6	Q9NZH6 homo sapien
8	210	25.3	218	4	Q9HBF3	Q9HBF3 homo sapien
9	201	24.2	164	4	Q9NZH7	Q9NZH7 homo sapien
10	185.5	22.3	155	4	Q9UBH0	Q9UBH0 homo sapien
11	184	22.2	267	13	Q73909	Q73909 gallus gall
12	183.5	22.1	159	4	Q9G6D6	Q9G6D6 homo sapien
13	180.5	21.7	176	6	Q9BEH0	Q9BEH0 canis fami
14	172.5	20.8	177	6	Q9GMZ4	Q9GMZ4 tursiops tr
15	170.5	20.5	176	6	Q9GKK2	Q9GKK2 canis fami
16	169	20.4	152	4	Q969H5	Q969H5 homo sapien

17	167.5	20.2	155	11	Q9QYY1	Q9QYY1 mus musculu
18	167.5	20.2	156	11	Q9JIG2	Q9JIG2 mus musculu
19	166.5	20.1	144	4	Q9BYX1	Q9BYX1 homo sapien
20	159.5	19.2	267	6	Q29082	Q29082 sus scrofa
21	154.5	18.6	260	13	Q9YGD3	Q9YGD3 oncorhynch
22	151.5	18.3	178	4	Q9HBF2	Q9HBF2 homo sapien
23	146	17.6	261	13	Q90W84	Q90W84 dicentrarch
24	144.5	17.4	283	13	Q9PVZ5	Q9PVZ5 xenopus lae
25	144	17.3	266	6	Q9TTK1	Q9TTK1 tursiops tr
26	143.5	17.3	153	4	Q43645	Q43645 homo sapien
27	143.5	17.3	269	4	Q96HE5	Q96HE5 homo sapien
28	138	16.6	272	13	Q9DDF2	Q9DDF2 cyprinus ca
29	136	16.4	267	11	Q91ZL5	Q91ZL5 sigmodon hi
30	136	16.4	276	13	Q57398	Q57398 cyprinus ca
31	136	16.4	276	13	Q9PW18	Q9PW18 cyprinus ca
32	133.5	15.1	272	13	Q9DDF3	Q9DDF3 cyprinus ca
33	124.5	15.0	254	13	Q9PT12	Q9PT12 oncorhynch
34	123.5	14.9	253	13	Q90W32	Q90W32 sparus aura
35	121	14.6	599	11	Q91WP7	Q91WP7 mus musculu
36	107	12.9	72	6	Q77771	Q77771 equus cabal
37	94	11.3	118	6	Q9TSJ0	Q9TSJ0 equus cabal
38	87	10.5	64	13	Q98SG5	Q98SG5 scopthalmu
39	82.5	9.9	65	6	Q9TV37	Q9TV37 equus cabal
40	81	9.8	256	10	Q9FX11	Q9FX11 arabidopsis
41	81	9.8	348	10	Q9FVW3	Q9FVW3 arabidopsis
42	79	9.5	747	5	Q9N9L5	Q9N9L5 leishmania
43	78	9.4	478	5	Q93759	Q93759 caenorhabdi
44	78	9.4	603	10	Q9SQT8	Q9SQT8 arabidopsis
45	76	9.2	728	4	Q9BRZ1	Q9BRZ1 homo sapien

## ALIGNMENTS

RESULT	1					
Q9UHA7						
ID	Q9UHA7	PRELIMINARY;	PRT;	158 AA.		
AC	Q9UHA7					
DT	01-MAY-2000 (TREMblrel. 13, Created)					
DT	01-MAY-2000 (TREMblrel. 13, Last sequence update)					
DE	01-DEC-2001 (TREMblrel. 19, Last annotation update)					
DE	FIL1 EPSILON.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=20092888; PubMed=10625660;					
RA	Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,					
RA	Sims J.E.;					
RT	"Four New Members Expand the IL-1 Superfamily.";					
RL	J. Biol. Chem. 275:1169-1175(2000).					
DR	EMBL; AF201831; AAF25211.1; -.					
DR	HSSP; F18510; IL1R.					
DR	InterPro; IPR000975; Interleukin_1.					
DR	Rfam; RF00340; IL1; 1.					
DR	ProDom; PD002536; Interleukin_1; 1.					
DR	SMART; SM00125; IL1; 1.					
SQ	SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;					

Query Match 99.5%; Score 826; DB 4; Length 158;  
 Best Local Similarity 99.4%; Pred. No. 6.7e-81;  
 Matches 157; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEKALKIDTPQSGSIQDINHNRVWLQDTLAVPRKDRMSPVTIALISCRHVETLEKDRG	60
DB	1	MEKALKIDTPQSGSIQDINHNRVWLQDTLAVPRKDRMSPVTIALISCRHVETLEKDRG	60
QY	61	NPITYLGLNGLNLCIMCAKVGQDPTQLKEKDMDLYNQPEPVKSFLEYHQSQRNSTFES	120
DB	61	NPITYLGLNGLNLCIMCAKVGQDPTQLKEKDMDLYNQPEPVKSFLEYHQSQRNSTFES	120



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ID Q9UHA5 PRELIMINARY; PRT; 157 AA.
AC Q9UHA5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE FILI ETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL; AF201833; AAF25213.1; -.
DR HSSP; PI0749; 2MIB.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN1.
SQ SEQUENCE 157 AA; 17702 MW; 7A54F3D7557A3EE3 CRC64;

Query Match 46.3%; Score 384; DB 4; Length 157;
Best Local Similarity 49.0%; Pred. No. 2e-33;
Matches 71; Conservative 29; Mismatches 45; Indels 0; Gaps 0;

QY 10 PQRSGIQDINHRVWVLODQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLN 69
DB 9 PKSYAIRDSRQWVWVLSNSLIAPLSRSTKPVTLHLIACRDTFEDSKERGNVYLGIGK 68

QY 70 LNLCLCMCAKVGDPQTLQLEKDIMLYNQPEPVKSFLYHSQSGRNSTFESVAFPGWFI 129
DB 69 KDLCLFCAEQKPTQLQLEKDIMLYNQPEPVKSFLYHSQSGRNSTFESVAFPGWFI 128

QY 130 VSSEGGCPILITQELGKANTDFGL 154
DB 129 TSTSGQPIFLTKERGINTNTNFYL 153

RESULT 5
ID Q9D626 PRELIMINARY; PRT; 183 AA.
AC Q9D626;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 2310043N20RIK PROTEIN.
GN 2310043N20RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Teyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Yushaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009787; BAB26505.1; -.
DR HSSP; P01584; 1HTB.
DR MGD; MGI:1916927; 2310043N20RIK.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN1.
SQ SEQUENCE 183 AA; 20878 MW; A3ACE339FB96F02F CRC64;

Query Match 40.1%; Score 333; DB 11; Length 183;
Best Local Similarity 44.4%; Pred. No. 7.1e-28;
Matches 64; Conservative 25; Mismatches 55; Indels 0; Gaps 0;

QY 9 TPOGSIQDINHRVWVLODQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLN 68
DB 34 SPRNRYVHDSQWVWVLTGNTLTAVPASNNVKPVILSLIACRDTFQDYKKNLYLGLIK 93

QY 69 GLNLCLCMCAKVGDPQTLQLEKDIMLYNQPEPVKSFLYHSQSGRNSTFESVAFPGWFI 128
DB 94 NRNLFCFCCVCKPTQLQLEKDIMLYNQPEPVKSFLYHSQSGRNSTFESVAFPGWFI 153

QY 129 AVSSEGGCPILITQELGKANTDF 152
DB 154 ATSSIEROTIILTHQKGLVNTNF 177

RESULT 6
ID Q9UHA6 PRELIMINARY; PRT; 192 AA.
AC Q9UHA6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FILI ZETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL; AF201832; AAF25212.1; -.
DR HSSP; PI8510; 1ILIR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 192 AA; 21543 MW; 4AF584C81802F612 CRC64;

Query Match 25.3%; Score 210; DB 4; Length 192;
Best Local Similarity 36.7%; Pred. No. 1.2e-14;
Matches 54; Conservative 26; Mismatches 61; Indels 6; Gaps 4;

QY 10 PQRSGIQDINHRVWVLODQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLN 68
DB 31 PKKFSIHDDHKVLVDGSLNIAPDKNYIRPEIFFALAS--SLSSASAEKSPILLGVS 88

QY 69 GLNLCLCMCAKVGDP--PTQLQLEKDIMLYNQPEPV--KSFLYHSQSGRNSTFESVAFPG 125

```

Db 89 KGFECLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIFYRAQVGSNNMLESAAHPG 148  
QY 126 WFTAVSSEGGCPILITQELGKANTTDF 152  
Db 149 WFICTSCNCPNPGVTDKFNKKHIEF 175

RESULT 7  
Q9NZH6 PRELIMINARY; PRT; 218 AA.  
AC Q9NZH6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE INTERLEUKIN-1 HOMOLOG 4 (IL-1X PROTEIN) (INTERLEUKIN-1-RELATED PROTEIN LONG ISOFORM A).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
TX TISSUE=FETAL LUNG, FETAL TESTIS, FETAL B-CELL, AND FETAL COLON;  
RX MEDLINE=20209405; PubMed=10744718;  
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,  
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,  
RA Young P.R.;  
RT Identification and initial characterization of four novel members of  
RT the interleukin-1 family.;  
RL J. Biol. Chem. 275:10308-10314 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
TX TISSUE=COLON CARCINOMA;  
RC Manoj P.P., Mantovani A., Muzio M.;  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Yansura D.,  
RA Lewis L., Eigenbrot C., Henzel W.J., Vandlen R., Filvaroff E.;  
RT "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-1R $\alpha$ ";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF200496; AAF69252.1; -.  
DR EMBL; AF167368; AAG29344.1; -.  
DR EMBL; AF251118; AAG14420.1; -.  
DR HSSP; P18510; 1ILR.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
DR ProDom; PD002536; Interleukin\_1; 1.  
DR SMART; SM00125; IL1; 1.  
SQ SEQUENCE 218 AA; 24126 MW; 96E089310D2CEA68 CRC64;

Query Match 25.3%; Score 210; DB 4; Length 218;  
Best Local Similarity 36.7%; Pred. No. 1.4e-14;  
Matches 54; Conservative 26; Mismatches 61; Indels 6; Gaps 4;

QY 10 PQRGSIQDINHVRVWLQDQTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGNPIYLGLN 68  
Db 57 PKKFSIHQDQHKVLVLDGSLNLIAPDKNYIRPEIFFALAS--SLSSASAEKGPILLGVS 114  
QY 69 GLNLCIMCAKVGQD--PTLQLEKEDIMLYNQPEPV-KSFLFYHSQSGRNSTFESVAFPG 125  
Db 115 KGFECLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIFYRAQVGSNNMLESAAHPG 174  
QY 126 WFTAVSSEGGCPILITQELGKANTTDF 152  
Db 175 WFICTSCNCPNPGVTDKFNKKHIEF 201

RESULT 8  
Q9HBF3

ID Q9HBF3 PRELIMINARY; PRT; 218 AA.  
AC Q9HBF3;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE INTERLEUKIN-1-RELATED PROTEIN LONG ISOFORM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
TX MEDLINE=21066552; PubMed=11145836;  
RA Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,  
RA Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.;  
RT "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-1R $\alpha$ ";  
RL Cytochrome 13:1-7(2001).  
DR EMBL; AF251119; AAG14421.1; -.  
DR HSSP; P18510; 1ILR.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
DR ProDom; PD002536; Interleukin\_1; 1.  
DR SMART; SM00125; IL1; 1.  
SQ SEQUENCE 218 AA; 24138 MW; 76E09C35093DEA63 CRC64;

Query Match 25.3%; Score 210; DB 4; Length 218;  
Best Local Similarity 36.7%; Pred. No. 1.4e-14;  
Matches 54; Conservative 26; Mismatches 61; Indels 6; Gaps 4;

QY 10 PQRGSIQDINHVRVWLQDQTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGNPIYLGLN 68  
Db 57 PKKFSIHQDQHKVLVLDGSLNLIAPDKNYIRPEIFFALAS--SLSSASAEKGPILLGVS 114  
QY 69 GLNLCIMCAKVGQD--PTLQLEKEDIMLYNQPEPV-KSFLFYHSQSGRNSTFESVAFPG 125  
Db 115 KGFECLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIFYRAQVGSNNMLESAAHPG 174  
QY 126 WFTAVSSEGGCPILITQELGKANTTDF 152  
Db 175 WFICTSCNCPNPGVTDKFNKKHIEF 201

RESULT 9  
Q9NZH7 PRELIMINARY; PRT; 164 AA.  
ID Q9NZH7  
AC Q9NZH7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE INTERLEUKIN-1 HOMOLOG 2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
TX TISSUE=OSTEOCLASTOMA;  
RX MEDLINE=20209405; PubMed=1074718;  
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,  
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,  
RA Young P.R.;  
RT Identification and initial characterization of four novel members of  
RT the interleukin-1 family.;  
RL J. Biol. Chem. 275:10308-10314 (2000).  
DR EMBL; AF200494; AAF69250.1; -.  
DR InterPro; IPR000975; Interleukin\_1.  
DR SMART; SM00125; IL1; 1.  
SQ SEQUENCE 164 AA; 18521 MW; F0D2099F4A357A0A CRC64;

Query Match 24.2%; Score 201; DB 4; Length 164;

Query Match	22.3%	Score 185.5	DB 4	Length 155
Best Local Similarity	44.8%	Pred. No. 4.1e-12		
Matches 43	Conservative 13	Mismatches 35	Indels 5	Gaps 3
QY	61	NPYYGLNGLNCLMCAKVGDOPTLQLEKXIDMDLYNQEPYKSLFYHSQSGRNSTFES	120	
Db	55	SPVLVEQVGSQGLSCG-VGGEPTLTLEPVMILYELIGAKESKSFYFRDRMDLTSEES	113	
QY	121	VAPPGWFIAVSSEGGCPILITQ--ELG-KANTITDF	152	
Db	114	AAYPGWFELCTVPEADQPVRLTQLPENGWNAITDF	149	
RESULT 11				
073909		PRELIMINARY;	PRT;	267 AA.
ID	073909			
AC	073909			
DT	01-AUG-1998	(TREMBLrel. 07, Created)		
DT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)		
DT	01-OCT-2001	(TREMBLrel. 18, Last annotation update)		
DE	INTERLEUKIN-IBETA.			
GN	IL-IBETA OR IL1B.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Weiding K.C., Sick C., Kaspers B., Staeheli P.;			
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=LINE N;			
RA	Kaiser P., Rothwell L., Goodchild M., Bumstead N.;			
RT	"Chicken interleukin-1b: an evolutionary bridge between fish and mammals."			
RT	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; J15006; CAA75239.1; -.			
DR	EMBL; AJ245728; CAC04510.1; -.			
DR	HSSP; P18510; 1ILR.			
DR	InterPro; IPR000975; Interleukin_1.			
DR	InterPro; IPR003502; Interleukin_1_prop.			
DR	Pfam; PF00340; IL1; 1.			
DR	Pfam; PF02394; IL1_propep; 1.			
DR	ProDom; PD002536; Interleukin_1; 1.			
DR	SMART; SM00135; IL1; 1.			
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.			
DR	CHAIN 106 267			
FT	INTERLEUKIN-1BETA.			
SQ	SEQUENCE 267 AA; 29822 MW; 3EF72164E4D40B64 CRC64;			
Query Match	22.2%	Score 184;	DB 13	Length 267;
Best Local Similarity	32.7%	Pred. No. 1.1e-11;		
Matches 54	Conservative 25	Mismatches 66	Indels 20	Gaps 6
QY	4	ALKIDTPQGSQTQDINHRWVQLQDT-LIAV----PRKDRMSPTIALISCHVETLEKD	58	
Db	108	AFYRTSRQSFQIDFNQRCFYLESPTQLVAHQGSQSSQKRLNIALYRPR-----GP	161	
QY	59	RGN-----PYVLGDLNGLNCLMCAKVGDOPTLQLEKXIDMDLYNQEPYKSLFYHSQS	112	
Db	162	RGASGTGOMPVAIGKGVKIVMSVMSVSTSEPTQLIFADWMDINDSYF-ITPEIFGVPLDS	220	

AC	Q9GKK2;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

Search completed: June 20, 2002, 15:10:55  
Job time: 466 sec

